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SUMMARIES

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jhn, M.R.,	a,S., Baug	., Batr	Yue, H., Tang, Y.T., Lal, P., Reddy, R., Batra, S., Baughn, M.R.,	, Lal,P	g, Y.T.	, Tan	Yue, H.	AUTHORS
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Klausner, R.D., Collins, F.S., Wagner, L., Schemmen, C.M., Schuler, G.D.,
Altschul, S.E., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Lulyk, S.W.,
Villaion, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Towchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
p. 23180527
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Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri, M.A., Mastrian,S.D., McCloskey,J.C.
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramur
Sequencing Center (NISC),
Gaithersburg, Maryland;
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Strausberg, R.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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BC000664.1
                                                                                                                                                                                                                                                        through the I.M.A.G.E. Consortium/LLNL at: http://image.llr
Series: IRAL Plate: 5 Row: d Column: 14
This clone was selected for full length sequencing because
passed the following selection criteria: matched mRNA gi: 1
Location/Qualifiers
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Tissue Procurement: ATCC
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/tissue_type="Colon, adenocarcinoma"
/clone_Tib="NIH_MGC_15"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
                                                                                                                                                   /mol_type="mRNA"
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                                                                                                                                                                                                      organism="Homo
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2027 AGCAGAGGGCTCACATCTCCCCTCTGATTCCCCCATGCACATTGCCTTATCTCTCCCCA 2086	- A	Qy 947 CACAGAAGGAGTATGCATTTTGACGGGCCTTGGGCTTCAATGGCTTTGAAGAAAAGGGCAA 1006
6 / TGCTGGGATTACAGGGGTAAGCCACCGTGCCGGGCCCAAAGGGAAACTCTTGTGGGAGG 2	) p &	Qy 887 CATGTACATGCTGATCTGGGGCAAGTTTGTGCTGTACAAATATGTCACCTGTTGGCTGGT 946
07 TGGCCAGGCTGGTCTCGAACTCCTGACCGCAAAG	, p &	Qy 827 CATCACAGAAGACTATCTCCTCACTGAAGACTATGACAACCACCCCTTCTGGTTCCGCTG 886
847 GGCAGCCACCATGCCCAGCTAATTTTTGTATTTTCAGTAGAAACGGGATTTCACCACGT 19	D Q	Qy 767 TCTCAAGCGCCTGAGTCTGGGCCTTTTCTACCTAGTGGGCCTACACACTGCTCAGCCCCCA 826
787	Qy	QY 707 GCTGGTGCAGGGAGAGCTGATTGACATACCAGGAAAGATACCAAACAAGATCATTCCTGC 766
08	Db QY	Qy 647 CTCCTACTTCTATGGGGCCTTCTTGGTAGGGCCCCAGTTCTCAATGAATCACTACATGAA 706
67 GTGCCTCTGCTGCCAGCCAAGTCTTCATTTGGGGCCAAAGGGGAAACTTTTTTTT	D Q	Qy 587 CTCTGAGCAACAGAAATATGCCATACGTGGTGTTCCTTCC
07 CCTTTGCCCCARAGCAGAATGGAAAAGCCAGGGAGGTGGAAGATCGATGCTTCCAGCT	Qγ	OY 527 GAAGCTGATTGGCTGTTGACTACTTTGACGGAAGGAAAGATCAGAATTCCTTGTC 586
47 28	Db Qy	Qy 467 TTACACTGCCACCGGCAACTACGATATCAAGTGGACAATGCCACATTGTGTTCTGACTTT 526
87 68	Db Oy	OY 407 CATCACTGCCGTCCTCACCTTTTGCTTCCAGATGGCCTACCTTCTGGCTGG
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	Qy Db	QY 287 CCACCTCTTCCATACCTTTACAGGCCTCTCAATTGCTTATTTTAACTTTTGGAAACCAGCT 346
88	Qy dd	Qy 227 GGGTTACCCCTTTGCTTTGTTTTATCGGCATTACCTTTTCTACAAGGAGACCTACCT
47 28	Ογ	Query Match 87.8%; Score 1996; DB 9; Length 2058; Best Local Similarity 100.0%; Pred. No. 0; Matches 2046; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1187 GGCCCTCTGGCACGGCCTGCACTCAGGATACCTGGTCTGCTTCCAGATGGAATTCCTCAT 1246	D Qy	CFOMKFLIVIVEROARLIQESPTLSKLAAITVLQPFYYLVQQTIHWLFMGYSMTAFC LFTWDKWLKVYKSIYFLGHIFFLSLLFILPYIHKAMVPRKEKLKKME"  875 c 457 g 556 t  ORIGIN
1127 CAAACGACTCAAGTTCCTTGGAAATAAAGAACTCTCTCAGGGTCTCTCGTTGCTATTCCT 1186 	Qy dg	KLIGLAVDYPDGGKDQNSLSSEQQKYAIRGVPSLLEVAGFSYFYGAFLVGPQFSMNHY MKLVQGELIDIPGKIPNSITEALKRLSIGLEYIVGYTLLSPHITEDYLLTEDYDNHPF WFRCMYMLLWGKFYLLYKYVTCWLVTBGVCILTGLGFNGFEEKGKAKWDACANMKVWLF ETNPRFTGTIASFNINTNAWYARYIFRRLKFLGNKELSQGLSLLFLLALWHGLHSGYLV
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1007 GGCAAAGTGGCGATGCCTGTGCCAACATGAAGGTGTGGTCTTTGAAACAAAC	Db Q	CDS 1771322 // Codon_start=1 // product="putative protein similar to nessy"
28 CACAGAAGGAGTATGCATTTTGACGGGCCTGGGCTTCAATGGCTTTGAAGAAAAGGGCAA	₽ ₽	gene 12058 /gene="C3F" /db xref."LocusID:10162"

. <b>Q</b>	Query Best Match	BASE CO	<b>FEATURES</b> <b>SOU</b>	AUTHORS TITLE TOURNAL COMMENT	TITLE	VERSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	RESULT 4 AK096775 LOCUS DEFINITION	4
47 GGGGGGTCCCTGTGGGGCTCCCCGGAGTTAAGATGGCGTCCTCAGCGGAGGGGGGACGAGGG 106	Query Match 82.2%; Score 1868; DB 9; Length 2482; Best Local Similarity 99.8%; Pred. No. 0; Matches 2208; Conservative 0; Mismatches 2; Indels 2; Gaps 2;	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="mRNA" /db_xref="mtaxon:9606" /clone="proST2010782" /tissue_type="prostate" /clone_tib="prOST2" /clone_tib="prOST2" /note="cloning vector: pME188FL3" COUNT 526 a 687 c 615 g 654 t	rce	Isogai, T. Direct Sub Submitted Submitted Kazusa-Kam (E-mail:ge NEDO human Economy, T	Sugiyama, T. irie, R.; Otsuki, T., Sato, H.; Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T. NEDO human cDNA sequencing project Unpublished	÷	2048 AAAAAAA 2054  4 AK096775 2482 bp mRNA linear PRI 15-JUL-2002 ION Homo sapiens cDNA FLJ39456 fis, clone PROST2010782, highly similar to Human C3f mRNA.	TCTAGCQJ          TCTAGCAC CTACCAC         CTACCAC CTACCAC TTTCTAC TTTCTAC AAAAAAAA
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	1067 CACTGGCACCATTGCCTCATTCAACATCAACACCAACGCCTGGGTGGCCCGCTACATCTT 1126	947 CACAGAAGGAGTATGCATTTTGACGGGCCTGGGCTTCAATGGCTTTGAAGAAAAAGGGCAA 1006	827 CATCACAGAAGACTATCTCCTCACTGAAGACTATGACAACCACCCCTTCTGGTTCCGCTG 886	707 GCTGGTGCAGGAGAGCTGATTGACATACCAGGAAAGATACCAAACAGCATCATTCCTGC 766	CTCTBAGCAACAGAAATATGCCATACGTGGTGTTCCTTCCCTGCTGGAAGTTGCTGGTTT	GALACTIGUES CONTROLL CONTROL CO	CCACCTCTTCCATACCTTACAGGCCTCTCAATTGCTTATTTTAACTTTGGAAACCAGCT CCACCTCTTCCATACCTTTTACAGGCCTCTCAATTGCTTATTTTAACTTTTGGAAAACCAGCT CTACCACTCCCTGCTGTGTATTGTGCTTCAGTTCCTCATCCTTCGACTAATGGGCCGCAC CTACCACTCCCTGCTGTGTATTGTGCTTCAGTTCCTCATCCTTCGACTAATGGGCCGCAC	

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                   TACATGAAGCTGGTGCAGGGAGAGCTGATTGACATACCAGGAAAGATACCAAACAGCATC
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-Lari,M.A., Shen,Y., Muzny,D.M., Lee,W. and Gibbs,R.A.
Submission
ted (24-SEP-1996) Molecular and Human Genetics, Baylor
ted of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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-Lari,M.A., Shen,Y., Muzny,D.M., Lee,W. and Gibbs,R.A. scale sequencing in human chromosome 12p13: experimental and actional gene structure determination
-Res. 7 (3), 268-280 (1997)
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corresponding genomic sequence in GenBank Accession Number
U72506"
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Qy 1059 CCCGGCTTCACTGGCACCATTGCCTCATTCAACATCAACACCAACGCCTGGGTGGCCCGC	ARCCAGCTCTACCACTCCCTGCTGTTATTGCTTCAGTTCTCAGTTCTCATCTCCACTAGTTAGT	Query Match  Best Local Similarity 100.0%; Score 1842; DB 9; Length 1842;  Best Local Similarity 100.0%; Pred. No. 0;  Matches 1842; Conservative 0; Mismatches 0; Indels 0; Gaps  Matches 1842; Conservative 0; Mismatches 0; Indels 0; Gaps  Qy 279 TACCTCATCCATCCATACCTTTACAGGCCTCTCAATTGCTTATTTTAACTTTTAGA  Qy 1
118  AXO73560 AXO7360 AXO73	Qy 1419 CITAMOGREPHANTICCATCHANTICCTROGCCACACCTTCTTCTCCCACCCTCCACTACTATTC Db 1141 CITAMOGREPHANTICCACACCACACTACTATTCCTTGCCCACACACTTCTTCTCCTAGACCACACTACTATTC 1479 ATATCCCTTATATTCCCTGGTGCCACACACTACTACTACTACTACTACTACTACTACTACTA	Qy 1299 AGCAAGCTGGCCGCCATTACTGTCCTCCAGCCCTTCTACTATTTGGTGCAACAGACCATC
linear PAT 06-FEB-2001; Vertebrata; Euteleostomi; ni; Hominidae; Homo.	ATCTTCTTCCTGAGCCTACTATTC 1478  ATCTTCTTCCTGAGCCTACTATTC 1200  ATAGAGAAGTTATAGAAGATGAAA 1538	TACTATTTGGTGCAACAGACCATC 1358

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                                               2 (bases 1 to 1573)
Sugano, S. and Suzuki,Y.
Direct Submission
Submitted (24-OCT-2001) Sumio Sugano, Institute of Medical Science,
Submitted (24-OCT-2001) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-549-5416)
                                                                                                                                                                                                                                                                                                                                                    AK058063.1 GI:16554077
oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NEDO human cDNA sequencing project supported by Ministry o Economy, Trade and Industry of Japan; cDNA full insert seq Research Association for Biotechnology (RAB); cDNA library
                                                                                                                                                                                                                                    Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S., Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S., Kusano,J., Watanabe,M., Eujimori,K., Tanai,H., Ishida,M., Yamashita,H., Chiba,Y., Suzuki,Y., Hata,H., Nakagawa,K., Mizuno, Morinaga,M., Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato, Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and
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Location/Qualifiers
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/note="cloning vector:
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TST00701"
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2 (bases 1 to 1146)

Ralnine,N., Chen,K., Rolfs,A., Halleck,A., Hines,L., Ei Kalnine,N., Chen,K., Rolfs,A., Moreira,D., Kelley,T., LaBaer Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer Phelan,M. and Farmer,A.

Direct Submission

Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 E Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full expression clones generated by BD Biosciences Clontech Harvard Institute of Proteomics. Each CDS has been clon
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens putative protein complete cds.
                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1146)

Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S. Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y. Phelan,M. and Farmer,A.

Cloning of human full-length CDSs in BD Creator(TM) System Donor
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tein,S., Lin,Y.,

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/db_xref="taxon:9606"
/clone="GH00356X1.0"
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e="Vector: pDNR-Dual"
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Direct Submission

Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Mea Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in t forms: with and without stop-codon (to allow fusion with C-tel
                                                                                                                                                                                                                                                                                                              artificial sequences.

1 (bases 1 to 1146)

Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Kalnine,N., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
Cloning of human full-length CDSs in BD Creator(TM) System Donor
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Synthetic construct Homo (Drosophila) mRNA, partia
                                                                                                                                                                    2 (bases 1 to 1146)
Kalnine, N., Chen, X., Rolf,
Koundinya, M., Raphael, J.,
Phelan, M. and Farmer, A.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGGCCGCACCATCACTGCCGTCCTCACTACCTTTTGCTTCCAGATGGCCTACCTTCTG 455
                                                                       CTCAGCCCCCACATCACAGAAGACTATCTCCTCACTGAAGACTATGACAACCACCCCTTC
                                                                                                                                           CACTACATGAAGCTGGTGCAGGGAGAGACTGATTGACATACCAGGAAAGATACCAAACAGC
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TGGTTCCGCTGCATGTACATGCTGATCTGGGGCAAGTTTGTGCTGTACAAATATGTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Homo sapiens putative protein similar to nessy (Drosophila)"
(Drosophila)"
/protein_id="hAP36403.1"
/db_xref="GI:30584309"
/translation="MGRFITAVLTTECFQMAYLLAGYYYTATGNYDIKWTMPHCVLTL
/translation="MGRFITAVLTTECFQMAYLLAGYYYTATGNYDIKWTMPHCVLTL
/translation="MGRFITAVLTTECFQMAYLLAGYYYTATGNYDIKWTMPHCVLTL
KLIGLAVDYFDGGKDQNSLSSEQQKYAIRGVPSLLEVAGFSYFYGAFLVGPCSMNHYY
MXLVQGELIDIFGKIPNSIIPALKRLSLGFYLJVGFYLLSGHAKWADACANNKVMLF
WRFCMYMLIMGKFVLYKYVTCWLVTEGVGLITCLGFNGFEEKGKAKWADACANNKVMLF
ETNPRFTGTIASFNINTNAWVARYIFKRLKEFLGNGELSLLFALMHGLHSGYLV
CFQMKFLIVIVERQAARLIQESFTLSKLAAITVLQFFYYLVQQTTHWLFMGYSWTAFC
LFTWDKWLKVYKSIYFLGHIFTLSLLFILPYIHKAMVPRKEKLKKMEL"
73 a 310 c 256 g 307 t
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/db_xref="taxon:32630"
/clone="GH00356L1.0"
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/codon_start=1
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note="Vector: pDNR-Dual"
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99.9%;
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AC006512 155975 bp DNA linear PRI 04-APR-2003 Homo sapiens 12 PAC RP3-461P17 (Roswell Park Cancer Institute Human PAC Library) complete sequence.
AC006512

VERSION AC006512.13 GI:29469488

KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 155975)

AUTHORS
AUZING, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bukey, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carzos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Chen, G., Chen, Z., Chiu, D., Dachorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Escotto, M., Falls, T., Ferraguto, D., Flaggy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (29-AUG-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA 9 (bases 1 to 155975)
                                                                                                                                                                         Direct Submission
Submitted (27-2000) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                        Submitted (18-707-1999) Human Genome of Molecular and Human Genetics, Bayl Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 5 (bases 1 to 155975)
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Baylor Plaza, Houston,
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QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
                                                                                                                                                                                                                                 SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 chones an reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality a region does not meet this standard, it will be indicated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are c sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
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STSs are identified using ePCR (Genome of a local database that includes entries local mapping efforts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Apr 2, 2003 this sequence version replaced gi:4926863 INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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9529. .957
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7675. .788
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12822. .12850
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1 (bases 1 to 22230)
Ansari-Lari,M.A., Muzny,D.M., Lu,J., Lu,F., Lilley,C.E., Spanos,S. Malley,T. and Gibbs,R.A.

Malley,T. and Gibbs,R.A.
A gene-rich cluster between the CD4 and triosephosphate isomerase genes at human chromosome 12p13
Genome Res. 6 (4), 314-326 (1996)
96303695
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Ansari-Lari,M.A., Shen,Y., Muzny,D.M., Lee,W. and Gibbs,R.A.
Large-scale sequencing in human chromosome 12p13: experimental
computational gene structure determination
Genome Res. 7 (3), 268-280 (1997)
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U47924 M86525 U72506
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                                                                                                                                                                                                                                                        Submitted (02-APR-1997) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Large-Scale Sequencing in Human Chromosome 12p13: Experimental Computational Gene Structure Determination.
                                                                                                                                                                                                                                                                                                                                                           Submitted (29-JAN-1997) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, US: (bases 1 to 222930)
Ansari-Lari,M.A., Shen,Y., Muzny,D.M., Lee,W. and Gibbs,R.A.
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Ansari-Lari,M.A., Shen,Y., Muzny,D.M., Direct Submission
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Genetics, Baylor College of Medicine, One Baylor Plaza, Houston.
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Ansari-Lari,M.A., Muzny,D.
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Direct Submission
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/rpt family="SVA"
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complement(11545.
/rpt_family="Alu"
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QKKS1QFHWKNSNQIKILGNQSSFLTKGSKLNDRADSRRSLNDQGNFPLIIKNIKLE
DSDTYIICEVEDQKEEVQLLVFGLTANSDTHLLGQGSLTLTLESBFGSSBSVQGRSFRIE
ENDTYIICEVEDQKEEVQLLVFGLTANSDTHLLGQGSLTIVLTESBFGSSBSVQGRSFRIE
KNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQ
VEFSFFLAFTVEKLTGSGELMWQAERASSSKSWITFDLKNKEVSVKRVTQDFKLQMGK
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
                                                                                                                                 Direct Submission
Submitted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                  Strausberg, R.
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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BC009856.1 GI:14602665
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Sequence tag and encoded
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BD023986.1 GI:22565209
JP 2001269182-A/232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey,
Greene, Mark Ketteman and Anuradha Madan
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through the I.M.A.G.
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VQLLHKLSVRAADGPQKLLKVIKNPVSDHFPVGCMKVGTSFSIPVVSDVRELVPSSDP
IVFVVGAFAHGKVSVEYTEKMVSISNYPLSAALTCAKLTTAFEEVWGVI"
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Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 232 02-OCT-2001;
                                                                                     CATCACTGCCGTCCTCACTACCTTTTGCTTCCAGATGGCCTA 448
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JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
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Ansari-Lari M.A., Muzny D.M., Lu J., Lu F., Lilley C.E., Spanos S.
Malley T., Gibbs R.A.;
Malley T., Gibbs R.A.;
Malley T., Spanos R.A.;
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Malley T., Lilley C.E., Spanos S.

Spanos Res. 6:314-326(1996).
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SEQUENCE FROM N.A. Shen Y., MANSARI-LARI M.A., Shen Y., MSubmitted (JAN-1997) to the EMBL; U72515; AAC51640.1; -.
                                                                              SEQUENCE FROM N.A. Ansari-Lari M.A., Shen Submitted (OCT-1996) to
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Ansari-Lari M.A., Muzr
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Ansari-Lari M.A., Shen Submitted (NOV-1996) to
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Q92g83 rickettsia
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Q9acd7 vibrio salm
Q77959 human immun
Q8cyq8 streptococc
Q97216 saccharomyc
Q95z10 homo sapien
Q8rpn0 ehrlichia c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8vav8 white spot
Q9udh5 homo sapien
Q8d6v0 leptospira
Q8d37 pyrococcus
Q9sq73 gossypium h
Q9sq74 gossypium h
Q8ed53 shewanella
Q9hap8 halobacteri.
Q9y628 homo sapien
Q8rr49 streptococc
                                                                                               R.A.;
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EMBL; U47924; AAB51326.1;

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RESULT

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Best Local S
Matches 381
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01-JUN-2001
01-MAR-2003
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                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ
EMBL; BC000664; AAH00664.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
Homo sapiens (Human)
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates;
                                                                                                                                                                            PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; Hypothetical protein.
SEQUENCE 381 AA; 44121 MW; 2BF19AB3
                                                                                                                                                                                                                                             InterPro; IPR001064; Crystallin.
InterPro; IPR004299; MBOAT_fam.
Pfam; PF03062; MBOAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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InterPro; IPR004299; MBOAT fam.
Pfam; PF03062; MBOAT; 1.
PROSITE; PS00225; CRYSTALLIN_BET
                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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381 AA; 44122 MW; FD2AFA6581551113 CRC64;
MGRTITAVLTTFCFQMAYLLAGYYYTATGNYDIKWTMPHCVLTLKLIGLAVDYFDGGKDQ
                       MGRTITAVLTTFCFQMAYLLAGYYYTATGNYDIKWTMPHCVLTLKLIGLAVDYFDGGKDQ
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ilarity 100.0%;
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Pred. No. 1.3e-284;
0; Mismatches 0;
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Pred. No.
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Matches 50
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O35131;
O1-JAN-1998 (TrEMBLrel. 0:
O1-JAN-1998 (TrEMBLrel. 0:
O1-JUN-2002 (TrEMBLrel. 2:
C3F (Fragment).
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Q8BNH6;
01-MAR-2003
Genome
                                            SEQUENCE FROM N.A.
MEDLINE=98112780; PubMed=9445485;
Ansari-Lari M.A., Oeltjen J.C., Schwartz S.,
Lu J., Gorrell J.H., Chinault A.C., Belmont
Gibbs R.A.;
                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF
          "Comparative sequence analysis of a gene-rich cluster at human chromosome 12p13 and its syntenic region in mouse chromosome 6 Genome Res. 8:29-40(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Unknown EST (Fragment).
Mus musculus (Mouse).
                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                   the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=Body; MEDLINE=22354683; PubMed=12466851; The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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50; Conserv
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(TrEMBLrel.
(TrEMBLrel.
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Conservative
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Sciurognathi; Muridae;
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annotation update)
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J.W., N
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                                                       y Z., Muzny
Miller W.,
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                                                                                                                           Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                            Team;
annotation
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                                                                                                                                                                                                                                                                                                 381
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Best Local :
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01-DEC-2001 (TrEMBLrel. 19, Last send)
01-UN-2002 (TrEMBLrel. 21, Last anno
Putative transmembrane protein PTG (1
MGC:11670).
Mus musculus (Mouse).
Eukaryota Metazoa; Chordata; Craniat
Mammalia; Eutheria; Rodentia; Sciurog
                                                                                                                                                                                                                                                                                                                                               Shen Y., Ansari-Lari M.A., Timms K.M., Yu W., Dugan S., L. Shen Y., Rowland K., Liu W., Perez L., Ding Y., Haywood M., Leal B., Logan O., Nguyen V., Savage L., Shen H., Worley K. Forcum J., Arenson A.D., Chiu M.W., Gorrell J.H., Brundage Chihault C., Nelson D., Gibbs R.A.; "Direct Submission."; Submitted (con ......")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q91V01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muzny D., Arenson A.D., Adams C., Brundage E., Bunac C., Carve Chacko J., Chen J., Di W., Ding Y., Dugan S., Durbin J., Forcu Ganesh R., Garcia C., Goodman M., Gorrell J.H., Haywood M., Hernandez J., Jackson L., Jin S., Kampal R., Karpathy S., Kova Leal B., Li Y., Lichtarge O., Liu W., Logan O., Lu J., Ly T., Leal B., Carve C., Oswal G., Perez L., Rashid N.D., Rowland K., Sava Scherer S.E., Shen H., Simon M., Stovall K., Timms K.M., Todd Vo Q., Williamson A., Worley K.C., Yu W., Chinault C., Nelson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Direct Submission.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases EMBL; AC003397; AAC36007.1; -.
                                                                                                                                                                                                                                                                                        Strausberg R. Submitted (AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                          SEQUENCE
                                                                                                                                                                                 Transmembrane
                                                                                                                                                                                                   InterPro; IPR004299; MBOAT_fam
Pfam; PF03062; MBOAT; 1.
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                           Similarity
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GTIASFNINTNAWVARYIFKRLKFLGNKELSQGLSLLFLALWHGLHSGYL
                                                                                                                                                                                                                                                                                                                                     FROM N.A.
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A
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Pred. No.
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                                                                      Mismatches
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annotation updat
TG (Unknown) (Property)
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, Haywood M., Jain A.,
H., Worley K., Chen E.,
Prundage E., Di W.,
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RESULT OF THE SULT OF THE SULT
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RA Addams M.D., Celniker S.E., Holt R.A., Sabburner M., Henderson S.N.,
RA Addams M.D., Celniker S.E., Holt R.A., Sabburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Zhang Q., Chen L.X.,
RA Burandon R.C., Rogers Y.H., Blazej R.G., Change M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.H., Blazej R.G., Change M., Pfeiffer B.D.,
RA Ballew R.M., Baynari A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beesley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolthakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolthakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPhorson D.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Murris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Murris J., Moshrefi A.,
RA Reinert K., Remigton K.S., Nurphy L., Muzny D.M., Nelseon D.,
RA Merkulov G., Standers R., Venter E., Wang A.H., Wang X.,
Ra Spier E., Spradling A.C., Stapl
                       Evans C.A.,
Banzon J., A
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Q961A6;
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Inse
Neoptera, Endopterygota, Diptera, Brachycera,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001
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NUMB OR CG3779.
                                                                                      SEQUENCE FROM N.A.
Celniker S.E., Adams
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An
                             Gocayne J.D.,
an H., Baldwin
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     Champe
                          Amanatides
D., Banzon
                                                                                      Kronmiller B., Wan K.H.,
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  P.G., Brandon R.C.
J., Beeson K.Y., I
Davenport L.B., Die
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era; Muscomorpha;
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A., Mungall C.J.,
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        Dietz
                                                                                Holt R.A.,
Rogers usam D.A.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Li p.W., Hoskins R.A., Galle R.F.,

Amanatides P.G., Scherer S.E., Li p.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

Man K.H., Agbayani A., An H.J., Andrews-Pfannkoch C.R., Baldwin D.,

Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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PROSITE; PS01179; PID; 1.
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RA Glodek A., Gong F. Gorrell J.H., Gu Z., Gulbart W.M., Glasser K.,
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibegwam C.,
RA Harris N.L., Howston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Lail M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Spier E., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
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RA Spiers E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., X, Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter E., Shu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.,
RI T'he genome sequence of Drosophila melanogaster.";
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A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Carlson J.W., Center V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Carlson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
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B., McIntosh T.C., Noy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
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Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Geoing R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Beyraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bartil J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
RA Beeson K.Y., Bence P.V., Berman B.P., Bandari D., Bolshakov S.,
RA Berkova D., Butlen M.R., Bouck J., Broakstein P., Brottlier P.,
RA Borkova D., Botchan M.R., Bouck J., Broakstein P., Brottlier P.,
RA Borlova D., Botchan M.R., Bouck J., Bavendale E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Borlova D., Botchar M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Harris N.L., Harvey D., Heinan T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heinan T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Keint C., Kravitz S., Kalp D., Lai Z.,
RA Hostin D., Houston K.A., Howland T.J., Wei M. H., Ibagwam C.,
RA Hostin D., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIncosh T.C., McLeod M.P., Mepherson D.,
Li Kake P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,
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Liu X., Mattei B., McIncosh T.C., McLeod M.P., Mepherson D.,
RA Meinert K., Remington K., Sanders R.D.C., Scheeber F., Shen H.,
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PROSITE; PS01179; PID;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
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                                                                                                                                                                                                                                                        FlyBase; FBgn0002973; numb
                                                                                                                                                                                                                                                                                  HSSP; P16554; 2NMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
                                  Local
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     Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELSOGLSLL
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     Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336
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                                                                                                                   60614 MW;
                                                                                                                                                                          ۳.
                                                                                                                                                                                                                           PTB_PID
1.8%; Score 9; DB 5
100.0%; Pred. No. 3.6
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13,
22,
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Last annotation updat
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                                                                                                                91B26959B5DE8405 CRC64;
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                            DB 5;
0. 3.6;
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Q9FXB7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9FXB7
Q9FXB7;
                                                                              Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Nguyen M., Lam B., Southwick A., Bei Buehler E., Chin Chiou J., Choi E., Dunn P., Gonzalez A., Howng B., Kim C., Koo T., Lee J.M., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Pham P., Sakano H., Schwartz J., Shinn P., Thaveri A., Toriumi M., Vaysberg M., Walker M., Yu G., Ecker J., Theologis A., Davis R.W.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; endicottyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                            EMBL; AC009323; AAG09097.1; InterPro; IPR005162; Retrot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F25P12.89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001584; Rve.
Pfam; PF03732; Retrotrans_gag; 1.
Pfam; PF00665; rve; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence features
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Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9FIC5;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9FIC5
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putative retroelement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB016892; BAB10837.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        physically assigned P1 and TAC DNA Res. 5:379-391(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tabata S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Asamizu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Columbia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.
Sequence features of the regions of 1,081,958 bp covered by seventeen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nterPro; IPR005162; Retrotrans_gag
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163504 MW; DA9700D7BFCB900B CRC64;
                          Retrotrans_gag
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Last annotation update)
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1462;
                                                                                                                                                                                               , Hansen N.F.,
Buehler E., Chin C.,
Kim C., Koo T.,
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Gaps

InterPro; IPR001878; Znf\_CCHC.

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RESULT 12
Q8WN94
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Matches 8
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Best Local S
Matches 9
                                                                                                                                                                               Q8WN94
Q8WN94;
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Q9GJX2;
                                                                                                                                        01-MAR-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U1-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2002 (TrEMBLrel. 21, Diazepam binding inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00939; C2HCZNFINGER.
SMART; SM00343; ZnF_C2HC; 1.
PROSITE; PS50158; ZF_CCHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF03732; Retrotrans gag; Pfam; PF00665; rve; 1. Pfam; PF00098; zf-CCHC; 1.
  Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00689; ACCABINDINGP. ProDom; PD002965; Ac coa bind PROSITE; PS00880; ACEP; I.
                  Eukaryota;
                                       Oryctolagus
                                                                                                                     01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AJ301367; CAC21172.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Davoli R., Fontanesi L., Zambonelli
Cenci V., Braglia S., Russo V.;
"Isolation and mapping of expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ301367; CAC
HSSP; P07107; 1ACA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polyprotein.
                                                                                Endozepine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   issue.
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                                                                            -MAR-2002 (TrEMBLrel. 20
-MAR-2003 (TrEMBLrel. 20
-MAR-2003 (TrEMBLrel. 20
-MAR-2003 (TrEMBLrel. 20
-/1-CoA-binding protein
-dozepine) (EP).
                                                                                                                                                                                                                                                                                                                                          308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pro; IPR000582; Ac_coA_bind_prot. PF00887; ACBP; 1.
                                                                                                                                                                                                                                                                                                       51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47
                                                                                                                                                                                                                                                                                                                                                                              Similarity
8; Conserv
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                                                                                                                                                                                                                                                                                                     KGKAKWDA
  Eutheria;
                                                                                                                                                                                                                                                                                                                                      KGKAKWDA 315
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cuniculus (Rabbit).
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
utheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                     88
                                                                                                                                                                                                                                                                                                                                                                                                                                                              8807 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                       1.6%;
                                                                                             20, Created)
23, Last sequence update)
23, Last annotation update)
n (ACBP) (Diazepam binding i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _bind_prot; 1.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                Score 8;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 9
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                                                                                                                                                                                                    PRT;
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Milc J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from
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                                                                                                 inhibitor)
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Sus.
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RESULT 13
Q9TSG2
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Best Local S
Matches
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Best Local S
Matches 8
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Q9TSG2;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                      TISSUB-Back Fat;
Ramli N., Suzuki H., Karnuah A.B., Hamasima N.
"Cloning of pig endozepine gene.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ
EMBL; AB019792; BAA34531.1;
HSSP; P07107; 1ACA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barmack N.H., Liu H., Qian Z., Bilderback T.;

"Localization of an endogenous diazepam ligand, acyl CoA binding protein, to Muller cells in rabbit retina.";

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: BINDS MEDIUM- AND LONG-CHAIN ACYL-COA ESTERS WITH VERY HIGH AFFINITY AND MAY FUNCTION AS AN INTRACELLULAR CARRIER OF ACYL-COA ESTERS. IT IS ALSO ABLE TO DISPLACE DIAZEPAM FROM THE BENZODIAZEPAME (BZD) RECOGNITION SITE LOCATED ON THE GABA TYPE A RECEPTOR. IT IS THEREFORE POSSIBLE THAT THIS PROTEIN ALSO ACTS AS A NEUROPEPTIDE TO MODULATE THE ACTION OF THE GABA RECEPTOR (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD002965; Ac_coA_bind_prot; 1.
PROSITE; PS00880; ACBP; FALSE_NEG.
Transport; Lipid-binding; Acetylation.
INIT_MET 0 0 BY SIMILARITY.
MOD_RES 1 1 ACETYLATION (BY SEQUENCE 86 AA; 9784 MW; F55EF76BB434AOF1
                                                                                                                                                                                                                                                                  NCBI_TaxID=9823;
[1]
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: MONOMER (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO THE ACBP
EMBL; AF407578; AAK98608.2; -
                                                                                                  SEQUENCE
                                                                                                             ProDom; PD002965; PROSITE; PS00880;
                                                                                                                                                InterPro; IPR000582; Ac_coA_bind_prot
Pfam; PF00887; ACBP; 1.
                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
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Pfam; PF00887; ACBP; 1.
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                                                                                                                                    PRINTS; PR00689; ACOABINDINGP.
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            Endozepine
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                       308
51
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                                               Similarity
8; Conserv
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8; Conserv
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KGKAKWDA
                       KGKAKWDA 315
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                                                Conservative
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Conservative (
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                                                                                                 A
58
                                                                                                             Ac_coA_bind_prot; 1. ACBP; 1.
                                                                                               9896 MW;
                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                           1.6%;
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13,
21,
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                                                                                                 3225B53E8307DE38 CRC64;
                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 8; DB 6
Pred. No. 7.6
0; Mismatches
                                                            Score 8;
Pred. No.
                                                Mismatches
                                                            DB 6;
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                                                Indels
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                                                                                                                                                                                                                                                                                         Euteleostomi;
Sus.
                                                                        87;
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RESULT 15
Q8W0Y
ID Q8W0Y
AC Q8
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                                                                                                      Query Match
Best Local S
Matches 8
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                                                                                                                                                                                                                               Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF463407; AAL68830.1; ... InterPro; IPR001087; Lipase GDSL. Pfam; PF00657; Lipase GDSL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8W0Y7
Q8W0Y7;
Q1-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thesis (2002), Department of Biozentrum Pharmacology/Neurobiology, University of Basel, Basel, Switzerland.
EMBL; AJ430511; CAD23129.1; -.
InterPro; IPR000582; Ac_coA_bind_prot.
Pfam; PF00887; ACBp; 1.
Probom; PD002965; Ac_coA_bind_prot; 1.
Probom; PD002965; Ac_coA_bind_prot; 1.
SEQUENCE 87 AA; 9805 MW; 67405B11C62AB066 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medicago truncatula (Barrel medic).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Jemalong;
Dickstein R., Hu X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENOD8.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enod8.3 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baader M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUR-2003 (TrEMBLrel. 23, Last annotation update)
Diagepam binding inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-broiler breeder; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Drug-Induction of Hepatic Cytochromes P450:
                                                                                                                                                                                                                                                                                                                                                                      Tandemly duplicated Enod8 genes are differentially expressed in ledicago.";
                                                                                                                                                                                                                                                                                                                                                                                                                     eung A.T.;
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                                                                                                y Match 1.6%; Score 8; DB:
Local Similarity 100.0%; Pred. No. 23
hes 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QUENCE FROM N.A.
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                                                 222 KIPNSIIP 229
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                                                                                                                                                                                                         AA; 33075 MW;
40
                                                                                                                                                                                                                                                                                                                                                                                                                                              Yang J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ba L.,
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                                                                                                                                                                                                            F2A7D59A499471AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Coque
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o. 7.7;
                                                                                                                            DB 10; Length 299;
5. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Kim D.-J., Cook D.R.,
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Search completed: November 21, 2003, 14:24:00 Job time : 42 secs

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Submitted (ApR-2001) to the EMBL,
EMBL; AY028317; AAK20915.1; -.
EMBL; BC006753; AAH06753.2; -.
InterPro; IPR004299; MBOAT_fam.
Pfam; PF03062; MBOAT; 1.
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SERAIN=C57BL/6J; TISSUE=Liver;
STRAIN=C57BL/6J; TISSUE=Liver;
Zhu Y., Han Y., Reddy J.K.;
Zhu Y., Han Y., Reddy J.K.;
"Cloning and initial characterization of mouse PTG cDNA, whose expression is in a PPAR alpha dependent manner.";
expression is in a PPAR alpha dependent manner.";
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Q91V01;
Q01P01;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-JÜN-2002 (TrEMBLrel. 21, Last annotation update)
Putative transmembrane protein PTG (Unknown) (Protein
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mus musculus (Mouse).
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MASTADGDMGETLEOMRGLWPGVEDLSLNKLATSLGASEQALRLIFSIFLGYPLALFYRH
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O1-JAN-1998
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C3F (Fragmen
Mus musculus
Muzny D., Arenson A.D., Adams C., Brundage E., Bunac C., Carvelli Chacko J., Chen J., Di W., Ding Y., Dugan S., Durbin J., Forcum J. Ganesh R., Garcia C., Goodman M., Gorrell J.H., Haywood M., Hernandez J., Jackson L., Jin S., Kampal R., Karpathy S., Kovar C. Leal B., Li Y., Lichtarge O., Liu W., Logan O., Lu J., Ly T., Leal B., Li Y., Lichtarge O., Liu W., Logan O., Lu J., Ly T., Martinez C., Oswal G., Perez L., Rashid N.D., Rowland K., Savage I Scherer S.E., Shen H., Simon M., Stovall K., Timms K.M., Todd J., Vo Q., Williamson A., Worley K.C., Yu W., Chinault C., Nelson D.,
                                                                                                                                                                                                                                        Muzny D., Ansari-Lari M.A., Timms K.M., Yu W., Dugan S., Shen Y., Rowland K., Liu W., Perez L., Ding Y., Haywood M Leal B., Logan O., Nguyen V., Savage L., Shen H., Worley Forcum J., Arenson A.D., Chiu M.W., Gorrell J.H., Brundag Chinault C., Nelson D., Gibbs R.A.; "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                            SEQUENCE FROM N.A. Muzny D., Arenson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98112780; PubMed=9445485;
AnBari-Lari M.A., Oeltjen J.C., Schwartz S.,
Lu J., Gorrell J.H., Chinault A.C., Belmont
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                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome
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Q1-FEB-1997
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C3F.
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Submitted (SEP-1998) to the EME
EMBL; AC002397; AAC36007.1; -
InterPro; IPR004299; MBOAT fam.
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Pred. No. 8.2e:
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RESULT
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                                  Malley T., Gibbs R.A.;
"A gene-rich cluster between genes at human chromosome 12p Genome Res. 6:314-326(1996).
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Ansari-Lari M.A.,
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Muzny D.M., Lu
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Primates;
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Q9BW40;
Q9BW40;
Q1-JUN-2001 (TrEMBLrel.
Q1-JUN-2001 (TrEMBLrel.
Q1-WAR-2003 (TrEMBLrel.
Q1-WAR-2003 (TrEMBLrel.
Hypothetical protein.
Homo sapiens (Human)
Strausberg R.;
Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ
EMBL; BC000664; AAH00664.1; -
InterPro; IPR001064; Crystallin.
InterPro; IPR004299; MBOAT fam.
Pfam; PF03062; MBOAT; 1.
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Ansari-Lari M.A., Shen Y., Muzny D.M., Lee W., Gibbs R. Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases EMBL; U72515; AAC51640.1; -.

EMBL; U77924; AAB51326.1; -.

InterPro; IPR001064; Crystallin.
InterPro; IPR004299; MBOAT fam.
Pfam; PP03062; MBOAT fam.
PFROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.

PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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TISSUE=Colon;
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Primates;
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Q8BNH6;
Q1-MAR-2003 (TYEMBLrel. 2:
01-MAR-2003 (TYEMBLrel. 2:
01-MAR-2003 (TYEMBLrel. 2:
Unknown EST (Fragment).
                                                                                                                                                                                                                                             EMBL; AKO
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE=Body;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research
"Analysis of the mouse transcriptome b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; Hypothetical protein.
SEQUENCE 381 AA; 44121 MW; 2BF19AB30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                   60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK083687; BAC38993.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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                                                                                                                                                               al Similarity
336; Conserv
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QKYAIRGVPSLLEVAGFSYFYGAFLVGPQFSMNHYMKLVRGQLTDIPGKMPNSTIPALKR
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89.8%;
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99.7%;
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20; Mismatches
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Pred. No. 1.2e-1
1; Mismatches
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0026630; nes.
InterPro; IPR004299; MBOAT fam.
                                                                                                                                                                                                                                                                                                                                                                                                                                "The evolutionary conserved gene nessy is a putative tay proteins in Drosophila embryo."; Submitted (FEB-199) to the EMBL/GenBank/DDBJ databases EMBL; AF128112; AAD28257.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9XYV9;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative transmembrane protein NESSY. NES OR NESSY OR CG9655.
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                       FWFRCMYMLIWGKFVLYKYVTCWLVTEGVCILTGLGFNGFEEKGKAKWDACANMKVWLFE
                                                          RRYKAFVDGEFRQHEGNVEAGV----RRFGAGAFYLIVCQVGLRYLPDSYFLTPEFAQVS
                                                                                                                                                                            GRDTYHSLIAILTTYFLVLLLRKKTQIFLAINFVFHMSYLLLGYFYTSSNDYDILMTMPH
                                                                                                                                                                                                                                                                  LNKLATSLGASEQALRLIISIFLGYPFALFYRHYL-FYKETYLIHLFHTFTGLSIAYFNF
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                                                                                      NHYMKLVQGELIDIPGKIPNSIIPALKRLSLGLFYLVGYTLLSPHITEDYLLTEDYDNHP
                                                                                                                     CILVLRMIGYGFDITDGLKEESELSKDQKETALKKPPSLLELLAFSYFPSGFLVGPQFPF
                                                                                                                                                CVLTLKLIGLAVDYFDGGKDQNSLSSEQQKYAIRGVPSLLEVAGFSYFYGAFLVGPQFSM
                                                                                                                                                                                                         GNQLYHSLLCIV-LQFLILRLMGRTITAVLTTFCFQMAYLLAGYYYTATGNYDIKWTMPH
                                                                                                                                                                                                                                     MDGIASGVGVPVEALRILLTILAGÝPVAALÝQKFISVIADKTVHHMFFAGCGAGLCYFNY
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   FVKRIYLLGFWAKFSLYKYISCWLLTEGALICIGLTYKGEDKNGQPDWSGCSNVKLKLLE
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Pred. No. 4.4e-66;
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                                              RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Golar R.P.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolishakov S.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerbalos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gerbalos B., Delcher A., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Gerbalos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.I., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.I., Harvey D., Helman T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liang Y., Lin X.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkilov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pecleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pecleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pecleb J.M.,
RA Melson D.R., Venter S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Merkilov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Smith T.,
RA Svirskas R., Tector C., Turner R., Venter J., Wang A.H., Wang X.,
RA Spier E.Y., 
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Q9VVX5;
01-MAY-2000
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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NES OR CG965
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01-JUN-2002
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                  SEQUENCE FROM N.A.
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Last annotation updat
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Best Local (
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                                                                                                                                                                                                    001925;
01-JUL-1997 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel. 101-MAR-2003 (TrEMBLrel. 1479othetical protein R155.1. Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-2001) to the EMBL/GenBank/DDBJ EMBL; AK003517; AAF49181.1; -
EMBL; AY070936; AAL48558.1; -
Flybase; FBgn0026630; nes.
InterPro; IPR004299; MBOAT fam.
Pfam; PF03062; MBOAT fam.
Pfam; PF03062; MBOAT; 1.
Pfam; PF03062; MBOAT; 1.
Pfam; PF03062; MSOAT; 1.
Pfam; PF03062; MSOAT; 1.

Pfam; PF03062; MSOAT; 1.

Pfam; PF03062; MSOAT; 1.

Pfam; PF03062; MSOAT; 1.

Pfam; PF03062; MSOAT; 1.

Pfam; PF03062; MSOAT; 1.
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                                                                               SEQUENCE FROM N.A. STRAIN=Bristol N2; MEDLINE=99069613;
                                                                                                                                                                      Eukaryota; Metazoa;
Rhabditidae; Peloder
                                                                                                                                                                                                                                                                                                                            001925
 "Genome sequence of the nematode C. elegans: a investigating biology. The C. elegans Sequencir Science 282:2012-2018(1998).
[2]
                                                                                                                                                    NCBI_TaxID=6239;
                                                                      Waterston
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||::| |:| |:: :: ::||:
MEYMVVSTEKQITRFYTKVVLPQWGHILNNSDIYKL-----LYFITLKSYNVVYMGW
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                                                                                                                                                                                                                                                                                                                                                                                                               CLTAFVFLKYERWIVVYGAVSYYGFTFLV
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(TrEMBLrel. 23, 1
(TrEMBLrel. 23, 1
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                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                        Peloderinae;
                                                                                    PubMed=9851916;
                                                                                                                                                                        Nematoda; Chromadorea; rinae; Caenorhabditis.
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Pred. No. 7.8e-66;
2; Mismatches 165
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RESULT

Q9V5F2

ID V5F2

ID V5F2

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Q9V5F2;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2002
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Submitted
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Hypothetical protein.
SEQUENCE 473 AA; 54111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Bristol N2;
Geisel C., Wamsley P., Kramer
"The sequence of C. elegans cc
submitted (MAY-1997) to the EM
                                                                                                                                                                                                                                    CG18445 protein.
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                                                                                                    SEQUENCE
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N2;
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STRAIN=BERKELEY;

MEDLINE=20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.

Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Henderson

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Inso
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 LATSLGASEQALRLIISIFLGYPFALFYRHYLFYKETYLIHLFHTFTGLSIAYFNFGNQL
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RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., Ann.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P. V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Rotchar R., Chandra I., Cadieu E., Center A., Chandra I., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies S.M., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M., RA Chandra I., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Houth N., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Howland T.J., Hernison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kilp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McShrefi A., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McShrefi A., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Alles R., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., P., Schen K., Rhoush J., Alles G., Ra, Rhall, Alles G., Ra, Ra, Marker G., Ra, Ra, M
                                                                                                                                                                                                                                                                                                                                                              YTLLSP--HITEDYLLTEDYDNHPFWFRCMYMLIWGKFVLYKYVTCWLVTEGVÇILTGLG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QAIHIAGLPAICYIVIRTQDPRIVQRAVLLVAMSYLLCVHLMRQLYDY-----GSYALDI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LATSLGASEQALRLISIFLGYPFALFYRHYLFYKE--TYLIHLFHTFTGLSIAYFNFGN 88
                                                              GTLLTFALSAVWHGFYPGYYLTFATGAVVVTAARTGRRLFRH----RFQSTQVTRMFYD
                                                                                                                     SQGLSLLFLALWHGLHSGYLVCFQMEFLIVIVERQAARLIQESPTLSKLAAITVLQPFYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LADMVGLSVDLVNFLICQISALFLASLFRSMLHPSKVSSKLRHTFALSIGLAFGYFCFGQ
      LVQQTIHWLFMGYSMTAFCLFTWDKWLKVYKSIYFLGHIFFLSLLFILP
                                                                                                                                                                                                                                        FNGFEEKGKAKWDACANMKVWLFETNERFTGTTASFNINTNAWVARYIFKRLKFLGNKEL
                                                                                                                                                                                                                                                                                                         FVKIYPVKDMKEDDFMNNTSMVYKYW----YAMMATTCIRFKYYHAWLLADAICNNSGLG
                                                                                                                                                                                                                                                                                                                                                                                                                            PLVFYKDYIEFVEGYNLLSTPPGNGNLDSSKREVVLEPSPTKAVIRKVVGSLVCAFIFMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TMPHCVLTLKLIGLAVDYFDG-GKDQNSLSSEQQKYAIRGVPSLLEVAGFSYFYGAFLVG
                                                                                                                                                                                FTGYDKDGNSKWDLISNINVLSFEFSTNMRDAINNWNCGTNRWLRTLVYERVP----QQY
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Fleischmann W.,
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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao O., Chen H., Cheu R.F., Chin C.W.,
RA Buehler E., Chan A., Chao O., Chen H., Cheu R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetkala I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzerg S.L., Schwattz J.R., Shinn P., Southwick A.M.,
RA Muterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                            "Arabidopsis Open Reading Frame (C
Submitted (JUN-2002) to the EMBL/C
EMBL; AC010795; AAG51612.1; -
EMBL; AY072080; AAL59903.1; -
EMBL; AY129979; AAM67512.1; -
InterPro; IPR001064; Crystallin.
InterPro; IPR004299; MBOAT_fam.
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A., Chang C.H., Dale J.M., Deng J.M., Hsuan V.W., Yamada K., Chan M.M., Chang C., Toriumi M., Mu'H.C., Yu G., Bowser L., Lee J.M., Quach H.L., Tang C., Toriumi X., Mu'H.C., Ya G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., ishida J., Jones T., Carninci P., Chen H., Cheuk R., Kawai J., Kim C., Lam B., Lin J., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9CAN8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M., Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jone Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozal Davis R.W., Ecker J.R., Theologis A.; "Pull Length cDNA of gene At1963050 (GI:15221667)."; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
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MEDLINE=21016719; PubMed=11130712;
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                                                          Pfam; PF03062;
PROSITE; PS0022
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                                                 03062; MBOAT; 1.
PS00225; CRYSTALLIN_BETAGAMMA; 1.
      465 AA;
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Last annotation update)
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      9A35E91B8277DCB3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Lin J.,
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밁 Ś 밁 Ś S

Query Match Best Local S Matches 121

Similarity

Score 408.5; Pred. No. 3.3

.3e-26;

Mismatches

Conservative

Pfam; PF03062; SEQUENCE 722

MBOAT; AA; 81

81221 MW; 15.8%; 89;

EMBL; AE003831; AAF58858.1; -. FlyBase; FBgn0033476; CG18445. FinterPro; IPR004299; MBOAT\_fam.

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369 362 313 302 257 244 197 201 137 142 82 89 22 31

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RESULT 11
042916
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                      Query Match
Best Local S
Matches 121
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Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                                                                                                                                          042916;
042916;
                                                                                    Wood V., Rajandream M.A., Barrell B.G., Beck A., Reinhardt Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AL021748; CAA16861.1; -. GeneDB SPombe; SPBC16A3.10; -. Interpro; IPR004299; MBOAT_fam. PF03062; MBOAT_fam.
                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                    Hypothetical
SEQUENCE 5
                                                                                                                                                 STRAIN=972h-;
Wood V., Raja
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    Hypothetical protein. SPBC16A3.10.
                                                                                                                                                                                                                                                                         01-JAN-1999 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                   01-JAN-1999 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
                                                                                                                                                                                           NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                          410
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                       121;
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                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSLNKLATSLGASEQALRLIISIFLGYPPALFYRHYLFYKETYLIHLFHTFTGLSIAYFN
ELSLNKLATSLGASEQALRLIISIFLGYPFALFYRHY------
                                                                                                                                                                                                                                                                                                                                                                               RKEE
                                                                                                                                                                                                                                                                                                                                                                                                     KKAME
                                                                                                                                                                                                                                                                                                                                                                                                                         -----VVLNYSSVGFMVLSLHETLVAFKSVYYIGTVIPIAVL-LLSYL-VPVKPVRPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                             QQTIHWLFMGYSMTAFCLFTWDKWLKVYKSIYFLGHIFFLSLLFILPYIHKAMVPRKEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VS----AVWHGLYPGYIIFFVQSALMIDGSKAIYRWQQAIPPKMAMLRNVLVLINFLYTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSLLFLALWHGLHSGYLVCFQMEFLIVIVERQAARLIQE-SPTLSKLAAITVLQPFYYLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKWDRAKNVDILGVELAKSAVQIPLFWNIQVSTWLRHYVYERIVKPGKKAGFFQLLATQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKWDACANMKVWLFETNPRFTGTIASFNINTNAWVARYIFKRLKFLGNKE-----LSQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTRFTEPVYQEWGFLKRFGYQYMAGFTARWKYYFIWSISEASIIISGLGFSGWTDETQTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDYLLTEDYDNHPFWFRCMYMLIWGKFVLYKYVTCWLVTEGVCILTGLGFNGF--EEKGK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHFAGPVFEMKDYLEWTEEKGIWAVSEKGKRPSPYGAMIRAVFQAAICMALYLYLVPQFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGGIDSTGALMVLTLKVISCSINYNDGMLKEEGLREAQKKNRLIQMPSLIEYFGYCLCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FG----FSSNLHFLVPMTIGYASMAIYRPLSGFITFFLGFAYLIGCHVFYMSGDAWK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGNQLYHSLLCIVLQFLILRLMGRTITAV-----LTTFCFQMAYLLAGYYYTATGNY--
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                                                                   509 AA;
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                       Conservative
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                             protein
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                                                                                                                                                                                                                                                                                                                                                                                                     487
                                                                   58821 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.8%; Score 407; DB 10; 25.4%; Pred. No. 2.6e-26; tive 90; Mismatches 227
                                 15.7%; Score 406;
25.1%; Pred. No. 3.
                                                                                                                                                                                                                                                                         23,
                     86;
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Last annotation updat
                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                       PRT;
                                                                  74B4E3E3D9DE65D9
                       Mismatches
                                                                                                                                                                                                                                                                                                                       509
                                 DB 3;
.5e-26;
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                                                                   CRC64;
                                           Length 509;
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                      Indels
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                      70;
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 -LFYKETYL
                      Gaps
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 69
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RESULT 12
Q08548
                    Query Match
Best Local Similarity
  Matches 133;
                                                                          EMBL; Z75083; CAA99384.1; -.
SGD; S0005701; YCR175C.
InterPro; IPR004299; MBOAT_fam.
Pfam; PF03062; MBOAT; 1.
SEQUENCE 619 AA; 72227 MW; 87C74C9194BE0BC5 CRC64;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Hughes B., Pohl T.M.;
Submitted (JUL-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2002 (TrEMBLrel. 21, Chromosome XV reading frame
                                                                                                                                                                              Submitted (JUL-1996)
                                                                                                                                                                                                                                                                                                                                                          Bordonne R., Camasses A., Madania A., Martin R.P., Tarassov I.A., Winsor B.;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 269-619 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q08548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q08548
                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
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                                                                                                                                                                                                                     EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPGFKSTLSTETVSAMMHGVSAGYYLTEVSAAFIQTVAKYTRRHVRPFFLKPDMETP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIGYNGLDSSKHPRWDRVKNIDPIKFEFADNIKCALEAWNWNTNKWLRNYVYLRVAKKGK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLGFNGFEEKGKAKWDACANMKVWLFETNPRFTGTIASFNINTNAWVARYIFKRLKFLGN 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLAAITVLQPF---YYLVQQTIHWLFMGYSMTAFCLFTWDKWLKVYKSIYFLGHIFFLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KE-LSQGLSLLFL-ALWHGLHSGYLVCFQMEFLIVIVERQAARLIQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LWLILFITGSSIYPLKFLLTPKFASSPILLKYGYVCITAFVARMKYYGAWELSDGACILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FYLVGYTLLSPHITEDYLLTEDYDNHPFWFRCMYMLIWGKFVLYKYVTCWLVTEGVCILT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYFLGYVFFFPSLLVGPAFDYVDYERFITLSMFKPLADPYEKQITPHSLEPALGRCWRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEVAGESYEYGAFLVGPQFSMNHYMKLVQ----GELIDIPGK--IPNSIIPALKRLSLGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IHLEHTETGLSIAYFN-----FGNQLYHSLLCIVLQFLILRLMGRTITAVLTTFCFQMAY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----PSENTDI--TASOMVICMKITAFAWSVYDGRIPSSELSSYOKDRAIRKIPNI 165
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457
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                                                                                                                                                                              to the
                    15.7%; Score 406; DB 3; 26.2%; Pred. No. 4.5e-26
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                                                                                                                                                                                                                                                             the
79;
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                                                                                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Mismatches
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                    4.5e-26;
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  238;
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                                     Length 619;
  Indels
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  58
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Gaps
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  17;
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28

LNKLATSLGASEQALRLIISIFLGYPFALFYRHY----LFYKETYLI--HLFHTFTGLSI 81

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RESULT
Q8RWH4
      ALD DE READER RE
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O1-OCT-2002 (TrEMBLrel.
Hypothetical protein.
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                                             Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda I Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Ka Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki Ecker J., Theologis A., Davis R.W.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY093087; AAM13086.1; -.

EMBL; AY128762; AAM91162.1; -.

EMBL; AY128762; AAM91162.1; -.

EMBL; DF03063, MBOAT fam.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                     InterPro; IPR004299; MBU. Pfam; PF03062; MBOAT; 1.
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Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
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Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
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Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen J
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Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watsson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LSQGLSLLFLALWHGLHSGYLVCFQMEFLIVIVERQAARLIQE-SPTLSKLAAITVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --DIKWIMPHCVLTLKLIGLAVDYFDGGKDQNSLSSEQQKYAIRGVPSLLEVAGFSYFYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSLNKLATSLGASEQALRLIISIFLGYPFALFYRHYLFYKETYLIHLFHTFTGLSIAYFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFLYTV-----LVLNYSAVGFMVLSLHETLTAYGSVYYIGTIIPVGLILLSYVVPAKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLLATQTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L--TRFTEPV----YQEWGFLRKFSYQYMAGFTARWKYYFIWSISEASIIISGLGFSGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFLVGPQFSMNHYMKLVQGELI------DIPGKIPNSIIPALKRLSLGLFYLVGYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDDASPKPKWDRAKNVDILGVELAKSAVQIPLVWNIQVSTWLRHYVYERLVQNGKKAGFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LISPHITEDYLLTEDYDNHPFWFRCMYMLIWGKFVLYKYVTCWLVTEGVCILTGLGFNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHFAGPVYEMKDYLEWTEGKGIWDTTEKRKKPSPYGATIRAILQAAICMALYLYLVPQYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGNQLYHSLLCIVLQFLILRLMGRTITAV-----LTTFCFQMAYLLAGYYYTATGNY--
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                                                                                                                                                                                                                                                                                                                                                                     Nematoda; Chromadorea; cinae; Caenorhabditis.
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Pred. No. 2.
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RESULT 15
Q9LN83
D9LN8
AC Q9LN8
AC Q9LN8
DT 01-OC
DT 01-UT
DE T12C
OS Arab
OC Spex
OC Spex
OC SPEX
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Best Local S
Matches 112
                                                                                                                                                                                                         Q9LN83;
Q9LN83;
01-OCT-2000
01-OCT-2000
01-UN-2002
T12C24.17.
SEQUENCE FROM N.A.

Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J. Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).

Bukāryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-1995) to the EMBL/GenBank/DDBJ EMBL; U40410; AAA81391.1; -. Wormbep; C5467.2; CE04270. Interpro; IPR004299; MBOAT_fam.
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
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24.1%; Pred. No. 2.7
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EMBL/GenBank/DDBJ databases
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                                                                        Kim C.,
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                                                         Lee J.,
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Best Local 9
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RKEE
                           RKEK
                                                                                 LVQQTIHWLFMGYSMTAFCLFTWDKWLKVYKSIYFLGHIFFLSLL---FILPYIHKAMVP
                                                                                                                           QGLSLLFLALMHGLHSGYLVCFQMEFLIVIVERQAARLIQE-SPTLSKLAAITVLQPFYY
                                                                                                                                                                                                                                                          ITEDYLLTEDYDNHPFWFRCMYMLIWGKFVLYKYVTCWLVTEGVCILTGLGFNGFEEKG-
                                                                                                                                                                                                                                                                                        PVYEMKDYLEWTEGKGIWDTTEKRKKPSPYGATIRAILQAAICMALYLYLVPQYPL--TR
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                                                                                                                                                                                                                                                                                                                                                                  WTMPHCVLTLKLIGLAVDYFDGGKDQNSLSSEQQKYAIRGVPSLLEVAGFSYFYGAFLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                   YHSLLCIVLQFLILRLMGRTITAV-----LTTFCFQMAYLLAGYYYTATGNY----DIK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAGSIGVSVAVLRFLLCFVATIPVSFACR---IVPSRLGKHLYAAASGAFLSYLSFG---
                                                       TV-----LVLNYSAVGFMVLSLHETLTAYGSVYYIGTIIPVGLILLSYVVPAKPSRPKP
                                                                                                               QTVS----AVWHGLYPGYMMFFVQSALMIAGSRVIYRWQQAISPKMAMLRNIMVFINFLY
                                                                                                                                                                       PKPKWDRAKNVDILGVELAKSAVQIPLVWNIQVSTWLRHYVYERLVQNGKKAGFFQLLAT
                                                                                                                                                                                                    -KAKWDACANMKVWLFETNPRFTGTIASFNINTNAWVARYIFKRLKFLGNKE-----LS
                                                                                                                                                                                                                               FTEPV----YQEWGFLRKFSYQYMAGFTARWKYYFIWSISEASIIISGLGFSGWTDDAS
                                                                                                                                                                                                                                                                                                                  PQFSMNHYMKLVQGELI------DIPGKIPNSIIPALKRLSLGLFYLVGYTLLSPH
                                                                                                                                                                                                                                                                                                                                                                                                          ----FSSNLHFLVPMTIGYASMÁIYRPKCGIITFFLGFÁÝLIGCHVFYMSGDAWKEGGID
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26.0%; Pred. No. 3.1e-24;
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Search completed: November 21, 2003, 14:16:0 Job time: 41 secs

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Database
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		5 871.5 33.8 6 638 24.7					Score
		.8 497 .7 128				į	F
24	222	22 21	22	22	22	21	
AB.T1 9323	ABB66994	ABB71792 AAG00235	ABG06198	AAB36584	AAB31669	AAY69987	ID
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AAB10902	AAB44681	ABP02154	ABP41674	ABB97427	AAB93101	AAU72495	ABP28284	ABG32098	ABB62100	ABG06197	ABG04834	ABP02013	ABG15613	AAM23923	AAM39872	ABG28291	AAM41658	ABG04835	AAB88563	ABG35460	AAM01438	AAM26088	AAM13688	AAM65826	AAM53449	ABB18117	ABB32619	ABB27468	ABG47472	ABB97850	ABB64492	AAG81345	AAB93797	ø	ABJ19324
S. xylosus DltB pr	uman secre	Human ORFX protein	ovari	Novel human protei	Human protein sequ	Arabidopsis partia	Streptococcus poly	ıΩ	ophila r	Novel human diagno	Novel human diagno	3	Novel human diagno		ü	Novel human diagno	₽		_	eptide	#120	#125	122	ie ma	rain e	#116	Peptide #125 encod	eptio	Human liver peptid		Drosophila melanog	ğ	protein	can	NOVX related prote

## ALIGNMENTS

AAY69987 standard; Protein; 487 AA.
ID AAY69987 standard; Protein; 487 AA.
XX AAY69987;
AC AAY69987;
XX DT 31-MAY-2000 (first entry)
XX XX AAY69987;
XX AAY69987;

Human receptor-associated protein from Incyte clone 2906971

Human receptor-associated protein; HRAP; Incyte clone 2906971; cytostatic; immunomodulatory; antiinflammatory; cardiant; antianaemic; antiarteriosclerotic; hepatotropic; antiarthritic antirhoumatic; antiasthmatic; osteopathic; antiallergic; antidabetic; dermatological; neuroprotective; diagnosis; treatment; prevention; reproductive disorder; cardiovascular; cell proliferative; autoimmune; inflammatory; allergy; gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS; arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis; multiple sclerosis; irritable bowel syndrome.

## XX AX AAY69987; XX XX AC AAY69987; XX XX XX AD 31-MAY-2000 XX Human recepto XX XX XX XX Human recepto XX Antiasthmatic Antiarticis; Antiasthmatic XX XX XX Homo sapiens XX XX XX Key FT Modified-site FT Modified-site

Key	Locatio	Location/Qualifiers	78	
Modified-site	ω		•	
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Modified-site	183		,	
	/note=	"Potential	'note= "Potential phosphorylation site"	site"
Modified-site	149			
	/note=	"Potential	'note= "Potential phosphorylation site"	site"
Modified-site	235			
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiinflammatory, cardiant, antiarteriosclerotic, hepatotropic, antiarthritic, antirheumatic, osteopathic, antialergic, antianemic, antialettic, dermatological and neuroprotective activities. The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with HRAP expression, especially cell proliferative, autoimmune/inflammatory, reproductive, cardiovascular and gastrointestinal disorders (e.g. atherosclerosis, cirrhosis, leukaemia, cancer, AIDS, arthritis, allergies, anaemia, asthma, dermaticis, diabetes, osteoporosis, multiple sclerosis and asthma, dermaticis, diabetes, osteoporosis, multiple sclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-AUG-1998;
01-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is expressed in nervous, gastrointestinal and reproductive tissues. HRAP has cytostatic, immunomodulatory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Pages 73-74; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human receptor-associated proteins (HRAP) useful for the diagnosis, treatment and prevention of cell proliferative, autoimmune, inflammatory, reproductive, cardiovascular, and gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillman JL, Yue H, I Corley NC, Baughn MR;
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                                                                                GFNGFEEKGKAKWDACANMKVWLFETNPRFTGT1ASFNINTNAWVARYIFKRLKFLGNKE
                                                                                                                                                                                                                                                                                 VPSLLEVAGFSYFYGAFLVGPQFSMNHYMKLVQGELIDIPGKIPNSIIPALKRLSLGLFY
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                                                                                                                                                                                             LVGYTLLSPHITEDYLLTEDYDNHPFWFRCMYMLIWGKFVLYKYVTCWLVTEGVCILTGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is a human receptor-associated protein lone 2906971 obtained from THYMNOT05 cDNA library.
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Query Match
Best Local Similarity

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Score 2580; DB 22; Pred. No. 5.5e-275;

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                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a human protein with hydrophobic domains. The protein possesses a hydrophobic domain and so is a secretory protein or a membrane protein. The protein is used as an antigen to prepare antibodies. The polynucleotide sequence is useful as a source of probes for genetic diagnosis. It is also useful for producing the protein in large quantities and for gene therapy. The eukaryotic cells are used for detecting the receptors or ligances corresponding to the protein and for detecting small novel pharmaceuticals. The antibodies are also used for detection, quantification and purification of the proteins. Both the protein and polynucleotide may be used in research or as nutritional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; hydrophobic protein; secretory protein; membrane protein; sepsis; tumour inhibition; immune deficiency; autoimmune disorder; anaemia; burn infectious disease; cancer; ulcer; periodontal disease; coagulation; parkinson's disease; fertility; immune response; thrombosis.
                                                                                                                                                           sources or supplements. The protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, hematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity and tumour inhibition activity. It may therefore may be used to treat immune deficiencies resulting from autoimmune disorders or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
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                                                             infectious diseases, cancer, sepsis, anaemias, burns and ulcers, periodontal disease, Parkinson's disease, induce fertility, imprimmune response and enhance coagulation or inhibit thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated human proteins and polynucleotides are used in research and have activities including cell proliferation/differentiation activity immune stimulating activity and receptor/ligand activity -
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14-MAY-1999;
                                                                                                                                                                                                                                                              Human; FLEXHT; full-length molecules expressed in human tissue; diagnosis; gene expression; genetic linkage; genetic variability; antianaemic; anticonvulsant; antiarteriosclerotic; immunomodulatory; cytostatic; antiathmatic; antiinflammatory; hepatotropic; antidiabetic; anti-gout; antithyroid; neuroprotective; antiarthritic; osteopathic; antipsoriatic; antixheumatic; antiulcer; gene therapy; anaemia; gout; epileps; arteriosclerosis; atherosclerosis; developmental disorder; cancer; immunological disorder; asthma; bronchitis; cirribosis; crohn's disease; diabetes mellitus; Grave's disease; multiple sclerosis; costeoarthritis; pancreatitis; rheumatoid arthritis; psoriasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC expressed in human tissues) proteins given in AAB36579 to AAB36633. The CC expressed in human tissues) proteins given in AAB36579 to AAB36633. The CC present invention describes an isolated polypeptide (A) comprising an CC amino acid sequence selected from one of 55 amino acid sequences 42-876 cC residues in length, corresponding to FLEXHT-1 to FLEXHT-55, a 90 % CC identical sequence, and a biologically active or immunogenic fragment of the sequence. The FLEXHT proteins can have antianaemic, anticonvulsant, CC antiinflammatory, hepatotropic, antidiabetic, antisportatic, antiuleer and antirheuratic activities, and can be used in gene therapy. The CC and antiinflammatic activities, and can be used in gene therapy. The CC polynucleotide sequences can be used to express the protein sequences. CP pharmaceutical compositions comprising FLEXHT can be used to treat disorders including anaemia, epilepsy, arteriosclerosis, cronis disease, developmental disorders, cancers, and immunological CC treat disorders such as asthma, bronchitis, cirrhosis, Cronis disease, CC diabetes mellitus, gout, Grave's disease, multiple sclerosis, and collecterities, and cronisis, pancreatitis, psoriasis, rheumatoid arthritis, and
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                                                                                       GFNGFEEKGKAKWDACANMKVWLFETNPRFTGTIASFNINTNAWVARYIFKRLKFLGNKE
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                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and CC polynepstide (II) sequences. (I) is useful as hybridisation probes, CC polynerase chain reaction (PCR) primers, oligomers, and for chromosome CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) and its binding partners are useful in medical. CC (Inaging) of sites expressing (II). (I) and (II) are useful for treating CC (Inaging) of sites expressing (II). (I) and (II) are useful for treating CC (Inaging) of sites expressing (II). (I) and (II) are useful for treating CC (Inaging) of sites expressing (II). (I) and (II) are useful for treating CC (Inaging) of sites expressing (II). (I) and (II) are useful for treating CC (Inaging) of sites expressing (II). (I) and (II) are useful for treating CC (II) and (II) are useful for treating
                                                               Query Match
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                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20;
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23-AUG-2000; 2000US-0649167.
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medical imaging; diagnostic; genetic disorder.
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                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                       Disclosure; SEQ ID NO 42168; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                     New isolated nucleic a
genes from Drosophila
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11-JUL-2000;
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                 WPI; 2001-656860/75
N-PSDB; ABL11097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) is obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and diagnostic, forensic, gene therapy and chromosome mapping proce
                                                                                                                                                                                                                                                                                                                                                                                                                       ABB66994 standard; Protein; 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; SEQ ID 4316; 71pp + CD-ROM; English
                                                                                                                    23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                             27-SEP-2001
                                                                                                                                                                                                                           WO200171042-A2
                                                                                                                                                                                                                                                       Drosophila melanogaster
                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide; \operatorname{pharmaceutical}.
                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 27774.
                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAC00241.
                                                                                        (PEKE ) PE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MASSAEGDEGTVVALAGVLQSGFQELSLNKLATSLGASEQALRLIISIFLGYPFALFYRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLFYKETYLIHLFHTFTGLSIAYFNFGNQLYHSLLCIVLQFLILRLMGRTITAVLTTFCF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MASSAEGDEGTVVALAGVLQSGFQELSLNKLATSLGASEQALRLIISIFLGYPFALFYRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLFYKETYLIHLFHTFTGLSIAYFNFGNQLYHSLLCIVLQFLILRLMGRTITAVLTTFCF
                                                                                        CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 AA;
                                                           Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                    2000US-191637P.
2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy and chromosome mapping procedures
                                                           Ŀ
                                                            PWD,
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Pred. No. 7.7e-62;
                                                           Myers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 128;
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genes from Drosophila interactions -

New isolated nucleic acid

acid detection reagent for detecting 1000 or more and for elucidating cell signalling and cell-cell

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RESULTS 7
AAU72527
ID AAU7
XX
AC AAU7
XX
C6-F
XX
C8 Arah
DE Arah
XX
C811
KW Plan
KW Plan
XX
XX
OS Arah
XX
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Best Local Similarity
                                                                                                                                                                                                                               AAU72527 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specification,
                  Arabidopsis thaliana
                                                                                     Cell cycle
                                                                                                                        Arabidopsis
                                                                                                                                                            26-FEB-2002
                                                  nutrient deprivation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                     424
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                                                               cycle protein; growth regular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82
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                                                                                                                                                                                                                                                                                                                     ILTCLITRVVLGYATFPFVLLEFMGSIKLYLRFYLCLHIISLVTIFILP 472
                                                                                                                                                                                                                                                                                                                                                                                                              SQGLSLLFLALWHGLHSGYLVCFQMEFLIVIVERQAARLIQESPTLSKLAAITVLQPFYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LADMVGLSVDLVNFLICQISALFLASLFRSMLHPSKVSSKLRHTFALSIGLAFGYFCFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LATSLGASEQALRLIISIFLGYPFALFYRHYLFYKE--TYLIHLFHTFTGLSIAYFNFGN
                                                                                                                                                                                                                                                                                                                                                                                       GTLLTFALSAVWHGFYPGYYLTFATGAVVVVTAARTGRRLFRH-----RFQSTQVTRMFYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FNGFEEKGKAKWDACANMKVWLFETNPRFTGTIASFNINTNAWVARYIFKRLKFLGNKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FVKIYPVKDMKEDDFMNNTSMVYKYW----YAMMATTCIRFKYYHAWLLADAICNNSGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YTLLSP--HITEDYLLTEDYDNHPFWFRCMYMLIWGKFVLYKYVTCWLVTEGVCILTGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLVFYKDYIEFVEGYNLLSTPPGNGNLDSSKREVVLEPSPTKAVIRKVVGSLVCAFIFMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGPLMIITQKVTSLAFSIHDGFVRGDEELTKAQQYHAIRKMPSALEYFSYVWHFQSILAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TMPHCVLTLKLIGLAVDYFDG-GKDQNSLSSEQQKYAIRGVPSLLEVAGFSYFYGAFLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QAIHIAGLPAICYIVIRTQDPRIVQRAVLLVAMSYLLCVHLMRQLYDY-----GSYALDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLYH-----SLLCIVLQFLILRLMGRTITAVLTTF--CFQMAYLLAGYYYTATGNYDIKW
                                                                                                                                                                                                                                                                                                                                                    LVQQTIHWLFMGYSMTAFCLFTWDKWLKVYKSIYFLGHIFFLSLLFILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTGYDKDGNSKWDLISNINVLSFEFSTNMRDAINNWNCGTNRWLRTLVYERVP----QQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQFSMNHYMKLVQG-ELIDIP---GKIPNS-----IIP----ALKRLSLG----LFYLVG
                                                                                                                        cell cycle protein CCP14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID
                                                                                                                                                          (first
                                                 rotein; CCP; cell cycle regulation; herbicide; regulator; plant development; abiotic stress; biotic rivation; pathogen attack; crop yield; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ata for this patent did not form part of the printed but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                               Protein; 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.8%; Score 408.5; DB 25.8%; Pred. No. 2e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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alling and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                   stress;
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138 61

EGGIDSTGALMVLTLKVISCSINYNDGMLKEEGLREAQKKNRLIQMPSLIEYFGYCLCCG -- DIKWTMPHCVLTLKLIGLAVDYFDGGKDQNSLSSEQQKYAIRGVPSLLEVAGFSYFYG 195 Ś

26

LSLNKLATSLGASEQALRLIISIFLGYPFALFYRHYLFYKETYLIHLFHTFTGLSIAYFN

FGNQLYHSLLCIVLQFLILRLMGRTITAV-----LTTFCFQMAYLLAGYYYTATGNY--LDMNSMAASIGVSVAVLRFLLCFVATIPISFLWR---FIPSRLGKHIYSAASGAFLSYLS

Query Match Best Local Matches

Similarity

15.8%;

Score 407; DB 23; Pred. No. 1.5e-35; Mismatches

Length 465;

44;

Gaps

60

Conservative

90;

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Copolypeptide and an anti-CCP antibody is useful for medulating the cell cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat, comaize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola.

CC cop nucleic acid and polypeptide molecules are useful as modulating to treat disorders characterised by insufficient or excessive production of ccp protein or production of ccp protein forms which have decreased or cof ccp polypeptide are useful as herbicides or plant growth regulators.

CC protein or production of ccp protein forms which have decreased or cf ccp polypeptide are useful as herbicides or plant growth regulators.

CC plant morphology, biochemistry and/or physiology, the length of the Gl, cs, G2 and/or w phase of the cell cycle of a plant, initiation, promotion, cs stimulation or enhancement of cell division, DNA replication, seed set, seed size, seed development, tuber, fruit, leaf formation, shoot and root initiation and/or development, tuber, fruit, leaf formation, shoot and root convironmental conditions, including abiotic stress such as pathogen attack, to modulate the cell cycle due to environmental conditions, including abiotic stress such as cold, mutrient deprivation, heat, drought, salt stress, or biotic cold, mutrient deprivation, heat, drought, salt stress, or biotic cold, mutrient deprivation, heat, drought, salt stress, or biotic cold, mutrient deprivation, heat, drought, salt stress, plant reproduction and seed development, endoreduplication in storage cells, cold stress such as gathogen attack, to modulate e.g. enhance crop yields, and attenuate plant architecture, plant quality traits, plant collis, cs storage tissues and/or storage organs of plants or its parts. CCP is useful for expressing CCP protein is oderect CCP mRNA, or a genetic cold lesion in a CCP gene and to modulate CCP activity. The present sequence crop calculation of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators -
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel cell cycle protein (CCP) and the polynucleotides encoding them. CCP is useful for identifying a cowhich modulates the activity of the polypeptide and which binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 34; Fig 14; 316pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAY-2000; 2000US-204045P
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     465 AA;
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                                                                                                                                                                                                                               04-JUN-2001;
06-JUN-2001;
                                                                                                                                                                                                                                                                                                                         WO200299062-A2
                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                      haematopoietic disorder; cancer; dyslipidaemia; metabolic disturbance; neurogenesis; cell differentiation; cell proliferation; haematopoiesis; wound healing; angiogenesis; gene therapy; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic; NOVX.
                                                                                                                                                                                                                                                                                                                                                                                                                        Antidiabetic; anorectic; virucide; antibacterial; fungicide; nootropi protozoacide; neuroprotective; antiparkinsonian; antilipaemic; NOVX-associated disorder; metabolic disorder; diabetes; anorexia; obesity; infectious disease; cancer-associated cachexia; immune disor neurodegenerative disorder; Alzheimer's disease; parkinson's disease; haematonidetic disorder; Cancer disdemias pratkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABJ19323
                                                                                                                                                                                                                                                                                                12-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antidiabetic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----VVLNYSSVGFMVLSLHETIVAFKSVYYIGTVIPIAVL-LLSYL-VPVKPVRPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKWDRAKNVDILGVELAKSAVQIPLFWNIQVSTWLRHYVYERIVKPGKKAGFFQLLATQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTRFTEPVYQEWGFLKRFGYQYMAGFTARWKYYFIWSISEASIIISGLGFSGWTDETQTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHFAGPVFEMKDYLEWTEEKGIWAVSEKGKRPSPYGAMIRAVFQAAICMALYLYLVPQFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQTIHWLFMGYSMTAFCLFTWDKWLKVYKSIYFLGHIFFLSLLFILFYIHKAMVFRKEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSLLFLALWHGLHSGYLVCFQMEFLIVIVERQAARLIQE-SPTLSKLAAITVLQPFYYLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDYLLTEDYDNHPFWFRCMYMLIWGKFVLYKYVTCWLVTEGVCILTGLGFNGF--EEKGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFLVGPQFSMNHYMKLVQGE----LIDIPGKIPNSIIPALKRLSLGLFYLVGYTLLSPHIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKWDACANMKVWLFETNPRFTGTIASFNINTNAWVARYIFKRLKFLGNKE-----LSQG
        2001US-295607P

2001US-296419A

2001US-296419A

2001US-296575P

2001US-297573P

2001US-297573P

2001US-298588P

2001US-298588P

2001US-298588P

2001US-298588P

2001US-298588P

2001US-398586P

2001US-3011530P

2001US-301550P

2001US-30154687P

2001US-3375244P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein SEQ
                                                                                                                                                                                                                                                                      2002WO-US17559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVWHGLYPGYIIFFVQSALMIDGSKAIYRWQQAIPPKMAMLRNVLVLINFLYTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                         disorder;
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á 밁 Ś 밁 Ś В S

215

NGKEETOYERTEPSPNSAV-VQKLLVCGLSLLFHLTICTT-LPVEYNIDEHFQATASWPT

-GK-----IPNSIIPALKRLSLGLFYLVGYTLLSPHITEDYLLTEDYDNHPFW-F

268

214 220

DE-ELTSSQRDLAVRRMPS

Matches 117; Query Match

113 96

AVLTTFCFQMA--YL----LAGYYYTATGNYDIKWTMPHCVLTLKLIGLAVDYFDG--GK 164

AIWFRTYLHSSKTSSFIRHVVATLLGLYLALFCFGWYALHFLVQSGISYCIMIIIG---V ALFYRHYLFYKET--YLIHLFHTFTGLSIAYFNFGNQLYHSLLCIVLQFLILRLMGRTIT

95

ENMHNYCFVFALGYLTVCQVTRVYIFDYGQYSADFSGPMMIITQKITSLACEIHDGMFRK

155

DQNSLSSEQQKYAIRGVPSLLEVAGESYFYGAFLVGPQFSMNHYMKLVQGELIDIP----

39 SS Local

Similarity

15.1%;

Score 389; DB 24; Pred. No. 1.7e-33; Mismatches

Length 520; Indels

Conservative

; 98

190;

56;

Gaps

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CC 86-1370 residue amino acid sequences, given in the specification, a
CC mature form of them, or a sequence that is at least 95 % identical to, or
CC having one or more conservative amino acid substitutions in one of the 36
CC amino acid sequences. The polypeptides, nucleic acid molecules and
CC antibodies of the invention are useful in the manufacture of a medicament
CC for treating a syndrome associated with a human disease, preferably a
CC NOVX-associated disorder. The nucleic acid molecules and
CC antibodies are useful for treating, preventing or diagnosing diseases
CC (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer-
CC associated cachexia, neurodegenerative disorders, Alzheimer's disease,
CC (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer-
CC aracious dyslipidaemias, or metabolic disturbances associated with
CC obesity, metabolic X syndrome, and wasting disorders. The nucleic acids
CC and polypeptides may also be used as targets for the identification of
CC small molecules that modulate or inhibit e.g. neurogenesis, cell
CC differentiation, cell proliferation, haematopoiesis, wound healing and
CC immunospecifically to NOVX substances for use in therapeutic or
CC diagnostic metabos. The nucleic acids are further used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine, and
CC invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-FEB-2002;
21-FEB-2002;
28-FEB-2002;
28-FEB-2002;
05-MAR-2002;
10-APR-2002;
10-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson
Shimkets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preventing, diagnosing or troobesity, cancer, Parkinson's various dyslipidemias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. obesity, cancer, Parkinson's disease, infections, immune disorders,
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polypeptide comprising any of the 36 86-1370 residue amino acid sequences, given in the specification, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; Page 101; 461pp; English.
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Miller CE,
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  520 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Zerhusen BD, Li L, Zhong M, Casman SJ, n
, Gorman L, Pena CEA, Kekuda R, Patturajan
Leite MW, Rastelli L, Macdougall JR, Taupie
Shenoy SG, Hjalt T, Voss EZ, Boldog FL, Ma
Ji W, Smithson G, Edinger SR, Millet I, E
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2002US-359151P.
2002US-361195P.
2002US-361964P.
2002US-371346P.
2002US-371523P.
2002US-0161493.
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FL, Malyankar UM;
t I, Ellerman K;
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          14-JUN-2001
15-JUN-2001
15-JUN-2001
21-JUN-2001
22-JUN-2001
28-JUN-2001
28-JUN-2001
28-JUN-2001
10-JUN-2001
11-SEP-2001
24-OCT-2001
14-DEC-2001
14-DEC-2001
14-DEC-2001
15-FEB-2002
21-FEB-2002
21-FEB-2002
10-APR-2002
11-APR-2002
11-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antidiabetic; anorectic; virucide; antibacterial; fungicide; nootropic; protozoacide; neuroprotective; antibarkinsonian; antilipaemic; NOVX-associated disorder; metabolic disorder; diabetes; anorexia; obesity; infectious disease; cancer-associated cachexia; immune disorder; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; haematopoietic disorder; cancer; dyslipidaemia; metabolic disturbance; neurogenesis; cell differentiation; cell proliferation; haematopoiesis; wound healing; angiogenesis; gene therapy; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic; NOVX.
                                                                                                                                                                                                                                                                                                                                          04-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                   04-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                           12-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOVX related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABJ19324 standard; Protein; 487
                                                                                                                                                                                                                                                                  12-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIVIVERQAARLIQES-----PTLSKLAAITVLQPFYYLVQQTIHWLFMGYSMTAFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RCMYMLIWGKFVLYKYVTCWLVTEGVCILTGLGFNGFEEKGKAKWDACANMKVWLFETNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSIKPSLTFYSSWYYCLHILGILVLLLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTWDKWLKVYKSIYFLGHIFFLSLLFILP 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFKMFLDNWNIQTALWLKRVCYERTSFSPTIQ----TFILSAIWHGVYPGYYLTFLTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFTGTTASFNINTNAWVARYIFKRLKFLGNKELSQGLSLLFLALWHGLHSGYLVCFQMEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIIYLYISLLAARPKYYFAWTLADAINNAAGFGFRGYDENGAARWDLISNLRIQQIEMST
                                                                                                                                                                                                                         2001US-297573P.
2001US-298285P.
2001US-298528P.
2001US-298556P.
                                                                                    2001US-341143P.
2002US-358643P.
                                                                                                             2001US-339266P.
2001US-337524P.
                                                                                                                                      2001US-318771P.
2001US-324687P.
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2001US-300177P.
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2001US-297567P.
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2001US-296418P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                              2001US-301550P.
2001US-302951P.
                                                                                                                                                                                                                                                                                                      2001US
                                                                                                                                                                                         2001US
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ASFNINTNAWVARYIFKRLKFLGNKELSQGLSLLFLALWHGLHSGYLVCFQMEFLIVIVE

**ISLLAARPKYYFAWTLADAINNAAGFGFRGYDENGAARWDLI** 

EMSTSFKMFL

305 334

IWGKFVLYKYVTCWLVTEGVCILTGLGFNGFEEKGKAKWDACANMKVWLFETNPRFTGTI QYERTEPSPNSAV-VQKLLVCGLSLLFHLTICTT-LPVEYNIDEHFQATASWPTKIIYLY -----IPNSIIPALKRLSLGLFYLVGYTLLSPHITEDYLLTEDYDNHPFW-FRCMYML

DNWNIQTALWLKRVCYERTSFSPTIQ----TFILSAIWHGVYPGYYLTFLTGVLMTL--

306

밁 á 밁 á

188

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밁

128

SSQRDLAVRRMPSLLEYLSYNCNFMGILAGPLCSYKDYITFIEGRSYHITQSGENGKEET SEQQKYAIRGVPSLLEVAGFSYFYGAFLVGPQFSMNHYMKLVQGELIDIP-----GK---

274

187 222 á

밁

Matches 109; Query Match Best Local Sequence

Similarity

14.1%;

Conservative

83;

Score 362.5; DB 24; Pred. No. 1.3e-30; 3; Mismatches 174;

24;

Indels Length

77;

Gaps

487 AA;

ALFYRHYLFYKET--YLIHLFHTETGLSIAYFNEGNQLYHSLLCIVLQFLILRLMGRTIT

AVLTTECEQMAYLLAGYYYTATGNYDIKWTMPHCVLTLKLIGLAVDYEDG--GKDQNSLS AIWFRTYLHSSKTSSFIRHVVATLLGLYLALFCFGWYALHFLVQSGISYCIMIIIG----

----VENMQPMMIITQKITSLACEIHDGMFRKDE-ELT

127 170

94

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for treating a syndrome associated with a human disease, preferably a NoVX-associated disorder. The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such as metabolic disorders, diabetes, obesity, infectious diseases (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer associated cachexia, neurodegenerative disorders, Albeimer's disease, parkinson's disease, immune disorders, haematopoietic disorders, cancer and various dyslipidaemias, or metabolic disturbances associated with obesity, metabolic x syndrome, and wasting disorders. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. This sequence represents a NOVX related protein of the
                                                                                                                                                                                                                                                                                                                                                                                               amino acid sequences. The polypeptides, nucleic acid molecules and antibodies of the invention are useful in the manufacture of a medicament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated polypeptide comprising any of the 86-1370 residue amino acid sequences, given in the specification, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preventing, diagnosing or tre
obesity, cancer, Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABT16023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spytek KA,
Miller CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; Page 102; 461pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Padigaru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2003-140607/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                    O residue amino acid sequences, given in the specification, a form of them, or a sequence that is at least 95 % identical one or more conservative amino acid substitutions in one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dyslipidemias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Zerhusen BD, Li L, Zhong M, Casman SJ, Gorman L, Pena CEA, Kekuda R, Pattura
Leite MW, Rastelli L, Macdougall JR, Tau
Shenoy SG, Hjalt T, Voss EZ, Boldog FL,
Ji W, Smithson G, Edinger SR, Millet I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infections, immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asman SJ, Patturajan M;
Te Taupier RJ,
Malyanke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           upier RJ, Guo >
  Malyankar UM;
, Ellerman K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders,
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RESULT 11
AAM93974
IID AAM93
XX AAM93
XX 13-NC
XX DT 13-NC
XX Human
XX Human
XX Human
XX Human
XX Homo
XX PPT 11-JA
PR 29-JU
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                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ota T, Ishii S, S
                                                                                                                                                                                                                                                                                                                         The invention relates to stomach cancer-expressed genes (AAI93842-AAI939). The (AAI93842-AAI939)17) and the encoded proteins (AAM93967-AAM94039). The genes can be used as markers in blood tests for screening for the early stages of the disease. The proteins and peptides can be used as targets for screening for compounds to treat the disease. They can also be used for predicting micro-metastases. The gene can predict peritoneal
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-FEB-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; stomach cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM93974 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stomach cancer-associated genes, useful as markers in screening for the early stages of the disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-570287/64.
DB; AAI93850.
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SQRDLAVRRMPSLLEYLSYNCNFMGILAGPLCSYKDYITFIEGRSYHITQSGENGKEETQ
                                         EQQKYAIRGVPSLLEVAGFSYFYGAFLVGPQFSMNHYMKLVQGELIDIP-----
                                                                                    FVFALGYLTVCQVTRVYIFDYGQYSADFSGPMMITQKITSLACEIHDGMFRKDE-ELTS
                                                                                                                              FCFQMAYL----LAGYYYTATGNYDIKWTMPHCVLTLKLIGLAVDYFDG--GKDQNSLSS
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Midorikawa
                                                                                                                                                                                                                                                                  432 AA;
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2000JP-0118776.

2000US-0183322.

2000JP-0183767.

2000JP-0241899.
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25.7%;
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                                                                                                                                                                       Score 334.5; DB 2
Pred. No. 1.3e-27;
'2; Mismatches 163
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A, Nagai K,
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                                                                                                                                                                           163;
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C, Otsuki
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                  The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence the complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a splynucleotide which comprises a 3'-end sequence, where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
oligonucleotide
                                                                                                                                                                                                                                                                                                      Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YERTEPSPNTAV-VQKLLVCGLSLLFHLTICTT-LPVEYNIDEHFQATASWPTKIIYLYI
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99JP-0300253
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T, Wakamatsu
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A, Nagai F
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                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; secretion; bacterial cell; fungal eukaryotic cell; fusion protein; maltose binding protein; immunoglobulin constant region; polyhistidine tag.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polypeptide for directing secretion of proteins of int from a host cell including, e.g. bacteria, includes contiguous acid residues of polypeptide with specified amino acids -
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                                                                                                                                                                                                   ABB64492 standard;
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                                                                                                               Drosophila melanogaster polypeptide
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                                                                                                                                                                                                                                                                                                    KVYKSIYFLGHIFFLSLLFILP 470
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Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capable of detecting 1000 or more genes from Drosophila. The invent: useful in developmental biology and in elucidating cell signalling & cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins

(ABB5737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid genes from Drosophila and interactions -
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
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)B; ABL08595.
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SSFGNIWRFYSSVYHIGYISWAAMTALGFYLTSQRKAAERRKKR
                                                                                                           RCWTFREGMKHWNVCVQYWLAVNVY---KLFPSKKYRTGATLLCSAYWHGFRPGHYFCIM
                                                                                                                                                                                             WLVTEGVCILTGLGFNGFEEKG------KAKWDA-----CANMKVWLFE
                                                                                                                                                                                                                                                                                                                                                                   AGYYYTATGNYDIKWTMPHCVLTLKLIGLAVDYFDGGKDQNSLSSEQQKYAIRGVP----
                                                                                                                                                                                                                                                                                                                                                                                                                           TGLSIAYFNFGNQLYHSLLCIVLQFLILRLMGRTITAV-----LTTFCFQMAYL----L
                        FTWDKWLKVYKSIYFLGHIFFLSLL---FILPYIHKAMVPRKEK
                                                      GAPFYVSLEDMWDKLVRKSATGTSRRVIDV
                                                                             MEFLIVIVERQAARLIQESPTLSKLAAITVLQPFYYLVQQTIHWLFMGYSMT----AFCL
                                                                                                                                     TNPRFTGTIASFNINTNAWVARYIFKRLKFLGNKELSQGLSLLFLALWHGLHSGYLVCFQ
                                                                                                                                                                TGLTLSECVCTMAGFGAYPDESDPNNGEGPRKRYQHLKRDADKHTYNFTTIVNTRVLEVE
                                                                                                                                                                                                                       ATLEKLKYAVFYCALYLATNYMWPLDYALSDEFFNDRSFVYRLLY--VWPTFFTFRARIY
                                                                                                                                                                                                                                                     A-LKRLSLGLFYLVGYTLLSPHITEDYLLTEDYDN-HPFWFRCMYMLIWGKFVLYKYVTC
                                                                                                                                                                                                                                                                               IEITDYDVELQSLSAAEILHYSFNYIGVLTGPYYRYRTYR-----DYFEMPFKTYAPTVE
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2000US-0614150
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Pred. No. 2.8e-17
3; Mismatches 19
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RESULT 15 ABB97850

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Stuart J, Jones AL,

Momiyama MG,

Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL; Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR; G, Bradley DL, Rohatgi SD, Harris B, Roseberry AM; Peralta CH, David MH, Panzer SR, Flores V, Daffo A; Chen AJ, Chang SC, Au AP, Inman RR;

Gerstin

Bradie, Dav Peralta CH, Dav

2002-315658/35. )B; ABL99847.

Polynucleotide sequences encoding human secretory proteins useful gene therapy of e.g. genetic deficiency disorders, cancers, and diseases caused by intracellular parasites -

Claim

29;

Page

430-431;

585pp;

English

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06-SEP-2000

06-SEP-2000
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05-SEP-2000;
05-SEP-2000;
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07-SEP-2000;
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06-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secretory protein; secretory polynucleotides; SPTM;
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                                                                                                                                                             INCYTE GENOMICS
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2000US-230896P.
2000US-230897P.
2000US-230951P.
2000US-231163P.
2000US-231832P.
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2000US-230519P.
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2000US-230596P.
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2000US-230599P.
2000US-230610P.
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2000US-230865P.
2000US-230988P.
2000US-230989P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention comprises the amino acid and coding sequences of human secretory (SPTM) proteins. The SPTM DNA and amino acid sequences are useful for treating a disease or condition associated with the expression of functional SPTM. The SPTM DNA sequences are useful for somatic or germline gene therapy to correct a genetic deficiency (e.g. severe combined immunodeficiency). The SPTM DNA sequences are also useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               providing protection against intracellular parasites (e.g. fungal parasites and protezoan parasites). The SPTM DNA and protein sequences are also useful for diagnosing cell proliferative disorders, cancer, immune disorders (e.g. AIDS), neurological disorders (e.g. Parkinson's immune of the control of the 
237 QAHTQRR 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                       414 TVLQPFYYLVQQTIHWLFMGYSMTAFCLFTWDKWLKVYKSIYFLGHIFFLSLLFILPYIH 473
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Perfect score:
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NADH2 dehydrogenas	T11739	N	355	4.1	106	<b>4</b> 5
-	T41664	N	537	4.1	106.5	4
	T13985	N	355	4.1	106.5	3
	T13984	N	355	4.1	106.5	2
	T13987	N	355	4.1	106.5	41
	T13919	N	355	4.1	106.5	0
	T19601	N	724	4.1	107	39
	T11314	N	619	4.1	107	8
	AD0885	N	392	4.1	107	37
	T11734	N	355	4.1	107	8
	T13908	2	355	4.2	107.5	35
	T13910	N	355		107.5	34
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hypothetical	H85958	N	392	4.2	109	õ

## ALIGNMENTS

20-Sep-1999 #text\_change 20-Sep-1999

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Meseidues: 1-486 <GEI>
A;Cross-references: EMBL:AF003390; NID:g2088866; PID:g2088868; PIDN:AAB54271.1; GSPDB:GNr
A;Experimental Bource: strain Bristol N2; clone R155 A;Map position: 3 A;Introns: 27/1; 127/2; 171/3; 203/2; 289/2; 324/2; 337/2; 439/3 367 151 KLIGLAVDYFDGGKDQNSLSSEQQKYAIRGVPSLLEVAGFSYFYGAFLVGPQFSMNHYMK 31 LATSLGASEQALRLIISIFLGYPFALFYRHYLFYKETYLIHLFHTFTGLSIAYFNFGNQL 90 91 YHSLLCIVLQFLILRLMGRTITAVLTTFCFQMAYLLAGYYYTATGNYDIKWTMPHCVLTL 150 RFIGLVMDVYDGAQKPEHLKPDQKLTAISDKPGLLEIAAFGLFFQGTLVGPQFTLSKFRS YNSVVESFNCGTNTFAKNONFAIFNIFATKIHİHRRLRWVNNKLASHVITLSYLAIWHGY WSWVTLWFRLTMYKYCAMWLITEGASILSGLGHNGKDAEGNDRWDGVRDLHIIKWETGHD CMYMLIWGKFVLYKYVTCWLVTEGVCILTGLGFNGFEEKGKAKWDACANMKVWLFETNPR 329 FVNGDWLDSDGQPPKSAFLPSIGRFLAGCTYMVLHQWGQFWIPDQYFNSDAYNNLSFFWR IHPILSIFGAFFITNFMAGTDASIYAAHIVFLGHLLIGYWFHETDTYDITWTTPFCIMTL HLGYFLLFGVELGCVQAQNQLYALIKRTPGWSEAISKPISRPFIWIFGKLTISYSMGFAF 426 HSGYLVCFQMEFLIVIVERQAARLIQESPTLSKLAAITVLQPFYYLVQQTIHWLFMGYSM 436 FTGTIASFNINTNAWVAR------YIFKRLKFLGNKELSQGLSLLFLALWHGL LSEVTSASEDALRILISVLAGYPLAVVHRTFFYNKPAQHQHLFFVIVGLSLWMFNCGSSV 66 95; Score 749.5; DB 2; Length 486; Pred. No. 5.7e-52; Mismatches Indels 23; Gaps 366 306 126 246

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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; De ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; M Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown protein, 29405-27288 [imported] - Arabidopsis thaliana (species: Arabidopsis thaliana (mouse-ear cress) C;Datc: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                          487
                                        465
                                                                                                             - VVLNYSSVGFMVLSLHETLVAFKSVYYIGTVIPIAVL-LLSYL-VPVKPVRPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.8%; Score 407; DB 2; 25.4%; Pred. No. 9.8e-25;
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Maiti, R.; Marziali
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                                                 probable membrane protein YOR175c - yeast (Saccharomyces N,Alternate names: hypothetical protein 03635 C;Species: Saccharomyces cerevisiae C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_C;Accession: S67067; S67063 R;Hughes, B.; Pohl, T.M. submitted to the Protein Sequence Database, July 1996 A;Reference number: S66685
A; Accession: S67067
A; Molecule type: DNA
A; Residues: 1-619 <H
                                                                                                                                                                                                       S67067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AL021748; PIDN:CAA16861.1; A;Experimental source: strain 972h-; cosmid c16A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-509 < WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number:
A;Accession: T39542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: T39542
R; Wood, V.; Rajandr
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Best Local :
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25.1%;
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#text\_change 19-Apr-2002

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hypothetical protein SPBC16A3.10 - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                    KE-LSQGLSLLFL-ALWHGLHSGYLVCFQMEFLIVIVERQAARLIQ------ESPTLS
                                                                                                                                                                                                                                                                                                              LWLILFITGSSIYPLKFLLTPKFASSPILLKYGYVCITAFVARMKYYGAWELSDGACILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELSLNKLATSLGASEQALRLIISIFLGYPFALFYRHY------LFYKETYL
                                              KLAAITVLQPF---YYLVQQTIHWLFMGYSMTAFCLFTWDKWLKVYKSIYFLGHIFFLSL
                                                                                                   RPGFKSTLSTFTVSAMWHGVSAGYYLTFVSAAFIQTVAKYTRRHVRPFFLKPDMETP---
                                                                                                                                                                                                           GIGYNGLDSSKHPRWDRVKNIDPIKFEFADNIKCALEAWNMNTNKWLRNYVYLRVAKKGK
                                                                                                                                                                                                                                                          GLGFNGFEEKGKAKWDACANMKVWLFETNPRFTGTIASFNINTNAWVARYIFKRLKFLGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGVHHLYDGVLVLLEDALFTYFVAAFYRSSRMPWIIFIV--ILGHTFSSHVIRYIY----
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GPFKRVYDVIGMVATNĹSLSYLIISFLLLNLKESIHVWKELYFIVHIYILIA
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Pred. No. 1.3e-24;
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C;Keywords: rransmembrane #status predicted <TM2>
F;53-69/Domain: transmembrane #status predicted <TM2>
F;461-477/Domain: transmembrane #status predicted <TM2>
                                                                                                                                           RESULT 5
T15839

RESULT 5
Apporthetical protein C54G7.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t.
C;Accession: T15839
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                  A; Molecule type: DNA
A; Residues: 1-480 < DUZ>
                                                                                                                                 R;Du, Z
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A;Map position: 15R
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A;Experimental source: strain S288C
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A; Residues: 270-619 <BOR>
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A; Accession: S67063
A;Crosstreferences: EMBL:U40410; NID:g1065453; PID:g1065454; PIDN:AAA81391.1; CESP:C54G7
                                               A; Status: preliminary; translated
                                                                 A; Accession: T15839
                                                                               A; Reference number:
                                                                                                 A; Description:
                                                                                                               submitted to the
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                                                                                                                                                                                                                                                                                                             LPY----IHKAMVPRK---EKLKKME
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                                                                                                                                                                                                                                                                             GPYAKQVTEFFKSKQPKEIFIRKQKKLE
                                                                                                                                                                                                                                                                                                                                         VTPLPSKKIYDLVGIYAIKLAFGYMVQPFIILDLKPSLMVWGSVYFYVHIIVAFSFFLFR
                                                                                                                                                                                                                                                                                                                                                                                                         GKKPGFRSTLFTFLTSAFWHGTRPGYYLTFATGALY----QTCGKIYRRNFRPIFLREDG
                                                                                                                                                                                                                                                                                                                                                                                                                                        GNKELSQGLSLLFL--ALWHGLHSGYLVCFQMEFLIVIVERQAARLIQES--PTLSKLAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TM----PHCVLTLKLIGLAVDYFDGG----KDQNSLSSEQQKYAIRGVPSLLEVAGFSYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTKIITNYGIDSFTLRYAICLLGSFPLNAILKRIPEKRIGLKCCFIISMSMFYLF----
                                                                               The sequence
                                                                                              EMBL Data Library, November 1995
ne sequence of C. elegans cosmid '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                  from
                                                                                                                                                       20-Sep-1999 #text_change 15-Sep-2000
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                                                                                                                                                                                                                            A; Gene:
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Best Local
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C;Genetics:
A;Gene: CESP:C54G7.2
A;Introns: 27/3; 76/2; 102/2; 185/3; 283/1; 384/3
C;Superfamily: Caenorhabditis elegans hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 IMVAVEKATMMAFNLKDGKAKDQSKLTEEQKRESLKEIPSLLEFMSFMFNFQTVLTGPAN 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEPLAETIGIEADRVNFVLSLFACFGISYVÝRKTCSLKQVNRQVRTVVPAVVGIGÍVFFC 73
                                                      GYSMTAFCLFTWDKWLKVYKSIYFLGHIFFLSLLFILPYIHKAM
                                                                                                                                                                                                                                                                        MKVWLFETNPRFTGTIASFNINTNAWVARYIFKRLKFLGNKELSQGLSLLFLALWHGLHS 378
                                                                                                                                                                                                                                                                                                                                                                                                                                          NYYDYIKFLDEKHLVADKHGKLPSPTGAAMKKFYQSLFFLAIVVTLGGKYKVED-VGTQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMNHYMKLVQGE--LIDIPGKIPNSIIPALKRLSLGLFYL-VGYTLLSPHITEDYLLTED 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HCVLTLKLIGLAVDYFDG-GKDQNSLSSEQQKYAIRGVPSLLEVAGFSYFYGAFLVGPQF 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNKLATSLGASEQALRLIISIFLGYPFALFYRHYLFYKET--YLIHLFHTFTGLSIAYFN
                                                                                                                                                               GYLVCFQMEFLIVIVERQAARLIQES-----PTLSKLAAITVLQPFYYLVQQTIHWLFM
                                                                                                                                                                                                                  VLPYQVEMAQSLKETLDGWNIQTGFWLRKVGYER----APKSIRTVATYTLSAVWHGVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGRAIKHLLANALGSYAIMYFAPPTQVHKIVLLFSMGYLFFIHCYRWAILESYSLDVTGP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGNQLYHSLLCIVLQFLILRLMGRT-ITAVLTTFCFQMAYLLAGYYYTATGNYDIKWTMP
AYATYSEVTMHMYPAYDVLKRVÝFIPHÍVAFAVIFALPKFFKPL
                                                                                                         GYYMAFFTCGLFTV----AAQTFRRSMRWRFLDDHNKKFAYDI---FSFIISK----IAL
                                                                                                                                                                                                                                                                                                                                                                                 YDNHPF--WFRCMYMLIWGKFVLYKYVTCWLVTEGVCILTGLGFNGFEEKGKAKWDACAN 318
                                                                                                                                                                                                                                                                                                                              YFALPFFQWFFWWFITIF--FIRCAYYFAWVFADAICNMSGFGFSGYDKEGNAEWKLCTN
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24.1%;
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Pred. No. 7.5e-23;
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A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-540 <WIL> C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence\_rev
C;Accession: T1997
R;Harris, B. RESULT 6 T19097 hypothetical protein C08F8.4 - Caenorhabditis elegans A;Map position: 4
A;Introns: 35/3; 82/2; 108/2; 146/3; 210/3; 309/1; 344/3; 411/3; C;Superfamily: Caenorhabditis elegans hypothetical protein CO8F8 A; Experimental source: clone C; Genetics: submitted to the EMBL Data A; Reference number: Z19073 ocal Similarity CESP: C08F8.4 TSVGLIFTYFCYGNAIAH-----LFINGFGSYLLMVSVPPQHVHKSVFAFAMGYLV 119 TFTGLSIAYENEGNQLYHSLLCIVLQELILRLMGRTITAV-----LTTECEQMAYLL 126 Conservative #sequence\_revision EMBL: Z73103; PIDN: CAA97423.1; GSPDB: GN00022; 11.5%; 25.0%; Library, C08F8 71; Score 297; DB 2; Pred. No. 6.6e-16; 1; Mismatches 171 from GB/EMBL/DDBJ Мау 15-Oct-1999 #text\_change Length 540; Indels 100; 15-Sep-2000 CESP:CO8F8.4 462/2; Gaps

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hypothetical protein F14F3.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t.C;Accession: T20899
R;Kershaw, J.
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T20899
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A;Map position: X
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A;Experimental source: clone F14F3
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                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                 GLSIAYENEGNQLYHSL----LCIVLQELILRLMGRTITAVLTTECEQMAYLLAGYYYTA 133
                                                                                                                                                         SPHITEDYLLTEDYDNHPFWFRCMYMLIWGKFVLYK--YVTCWLVTEGVCILTGLG----
                                                                                                                                                                                                                                                         VNEVASHTNVIQLIITLRIIGITFEENDAWVHKSDEN-----PTKRYLTELPTILEKFAY
                                                                                                                                                                                                                                                                                      TGNYDIKWTMPHCVLTLKLIGLAVDYFDG---GKDQNSLSSEQQKYAIRGVPSLLEVAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEKTGKPYDPTSTAMKKFEAAIAFSVVYTILGSYLPMS--LTNDPSINEY-----NLLIW
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                                                              ASNPKI IMGPTDLNAFDKLKTRENI EMSSDAI VNLDI PKVEFSDGFRDGMKAWNRSVQTW
                                                                                                                             NHYFPLDILRSDAIWEVSFFTRLVYAAL--IFVVFKTRVYSAWAIAESICVILGIGIYPA
                                                                                                                                                                                            FYHFCGLFTGPYYTYQ-----MLIDSQNPILKSWDPTLEVKSRFVRLLWSVPVFVIT
                                                                                                                                                                                                                        SYFYGAFLVGPQFSMNHYMKLVQGELIDIPGKIPNSIIPALK---RLSLGLFYLVGYTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NYKEMVDNWNIWTVAWLRRVVYERV------EGPYRTLAVYVTGAAWHGLAVGYYFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WLITVAASTVHRLPYYFAWTISDSICNISGFGYDGLADETLEPKWSRTTNVKPLLVEFGQ
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                                                                                                                                                                                                                                                                                                                       GFAMSLFIIGPKIVYSLGICSIAISIQ-LLANKKSTPLYVFLTTFTYLM-FVRFAHYILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --YVMHFWPS-LFMYRKLLMIPHFIALFIYLYLPQI 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLTSALFTLSAATFRRCMRHRFLGNSMHKL----MYDIFGMLVSKFAIGYIHWPF----
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                                                                                                                                                                                                                                                                                                                                                                                  9.5%; Score 244.5; DB 2;
21.3%; Pred. No. 8.7e-12;
ative 91; Mismatches 184;
                                                                                            FNGFE----EKGKAKWDACANMKVWLFETNPRFTGTIASFNINTNAW
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             membrane protein YOR175c homolog - barl
C;Species: Hordeum vulgare (barley)
C;Date: 09-Apr-1999 #sequence_revision
C;Accession: T05909
R;Hess, W.R.; Golz, R.R.; Boerner, T.
Plant Sci. 133, 191-201, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics
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A;Map position: 4
A;Introns: 35/3; 82/2; 108/2; 146/3; 191/3; 266/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C08F8.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:Z82287; PIDN:CAB05316.1; GSPDB:GN00022; CESP:ZK550.1 A;Experimental source: clone ZK550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-366 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein ZK550.1 - Caenorha C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, A; Reference number: Z20438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 6.1%; Score 158.5; DB 2; Local Similarity 21.6%; Pred. No. 4.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---YTATGNYDIKWTMPHCVLTLKLIGLAVDYFDGGK-DQNSLSSEQQKYAIRGVPSLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLSIAYFNFGNQLYHSLLCIVLQFLILRLMGRTITAVL-----TTFCFQMAYL-LAGYY 130
---EDPYRVIAVYVTGVAWHGLAVEYYLSFLTSAIFTLLAKVGSTLFQ----AIKMAANT
                                                  GNKELSQGLSLLFL--ALWHGLHSGYLVCFQMEFLIVIVERQAARLIQESPTLSKLAAIT
                                                                                                                                                                                                                 SSFCSALYSLLPIPLTKYPTISE------YNLL-----YNLL----
                                                                                                                                                                                                                                                                   GLFYLVGYTLLSPHITEDYLLTEDYDNHPFWFRCMYMLIWGKFVLYKYVTCWLVTEGVCI
                                                                                                                                                                                                                                                                                                                        FASYMFAFOSVIIGP---TNHYSNWSAYLDLKLVPKFERTGRPFDSTSTVFEKFKVAIAL
                                                                                                                                                                                                                                                                                                                                                                          VAGESYFYGAELVGPQFSMNHY------MKLV-QGELIDIPGKIPNSIIPALK-RLSL
                                                                                                                                                                                                                                                                                                                                                                                                                               RWIYQETYNLGFTGSMMVAVGKITLLSSAIT--DGMRSDLKALNSGQKRDAVNEIPSLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFIFLYFCYGNEIAHFFINGFGSYLLM-----ISVLPKHVHKAVFSFAMAYLFLVHFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIYYWLPLLCIPFYIYSAKISKPKKAQKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---FFLSLLFILPYIHKAMVPRKEKLKKME
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                                                                                                                                                         LTGLGFNGFEEKGKAKWDACANMKVWLFETNPRFTGTIASFNINTNAWVARYIFKRLKFL
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                                                                                                            -STNCNVW
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barley (fragment)

09-Apr-1999 #text\_change 08-Oct-1999

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RESULT 10

AE2313

hypothetical protein alr4060 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

A;Note: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C;Accession: AE2313

C;Accession: Nakammira Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2313
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A;Reference:number: 415411
A;Accession: TO5909
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Molecule type: DNA
A,Residues: 1-477 <KUR>
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
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Best Local S
Matches 85
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NA Res. 8, 205-213, 2001
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;Experimental source: cv. Haisa, leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Gene: alr4060
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;Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                          167
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                                                                                                                            287
                                                                                                                                                                                                                                                                     107 GLADNWQSKSIPGMGSIPPGLSFYTFQMVAFVVDSYTSRKKRAIGALDYLNFVSFFPQVV
                                                                                                                                                                                                                                                                                                                      168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392 IVERQAARLIQESPTLSKLAAITVLQPFYYLVQQTIH 428
333 TIASF----NINTNAWVARYIFKRLKFLG-NKELSQGLSLLFLAL---WHGLHSGYLVCF 384
                                                                                                                                                                                                                     228 IPALKRLSLGLFYLVGYTLLSPHITEDYLLTEDYDNHPFWFRCMYMLIWGKFVLYKYVT-
                                                                                                                                                                                                                                                                                                                                                                                                                    108 GRTITAVLTTFCFQMAYLLAGYYYTATGNYDIKWTMPHCVLTLKLIGLAVDYFDGGKDQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 EGVCILTGLGFNGFEEKG--KAKWDACANMKVWLFETNPRFTGTIA----SFNINTNAWV 345
                                                                       216 YIKLDQAQNPWLVWFFAFLFTLQIYFDFGGYSFIALGLAKF---LGINLTINFLAPYTSQ
                                                                                                                                                                                                                                                                                                                                                                        69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 RYYVYERLIQKGKKPGFLOLLGTQTVS-----AIWHGLYPGYMIFFVQSALMINGSK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EAAIIISGLGFTGWSDSSPPKAKWDRAINVDILGVE----LAGSAAQLPLKWNIQVSTWL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                   SLSSEQQKYAIRGVPSLLEVAGFSYFYGAFLVGPQFSMNHYMKLVQGELIDIPGKIPNSI 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FYKETYLIHLFHTFTGL-----SIAYFNFGNQLYHSLLC----IVLQFLILRLM 107
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                                                                                                                                                                                                                                                                                                                                                                      GWKAKAIATTVIIIDIAILAYFKYL---NFFVE-----DVLGLLVP------
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                                                                                                                                                                       AGPIERRG-DLF------PQI-ESFRFKFTYDNFETGFRWLSLGLFMKFVLADNISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FFTVRYVAKSLNLWRGIFDAVGLAAISSLLFVNASRSSFAIFVCEIIFNYVMVWLMLRQQ
                                                                                                                       -CWLVTEGVCILT-----GLGFNGFEEKGKAKWDACANMKVWLFETNPRFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.5%; Score 116.5; DB 2; 20.0%; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45;
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  RESULT 12
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Db Qy	B 8	B 8	용왕	B 8	B 8	₽ &	B &	B &	Query Ma Best Loo Matches	Qy 38  Db 33  Qy 43  Qy 43  Qy 43  Db 37  RESULT 11  C69451  C;Species: A C;Date: 05-D C;Accession: R;Klenk, H.P. ; Fleischma Glodek, A.; Nature 39 A;Authors: U Smith, H.O.; A;Title: The A;Reference A;Accession: A;Status: pr A;Molecule t A;Residues: A;Cross-refe	ę
422 LVQQTIHWLFMGYSMTAFCLFTWDK 446 -	372 LWHGLHSGYLVCFQMEFLIVIVERQAARLIQESPTLSKLAAITVLQPFYY 421	326 TNPRETGTIASFNINTNAWVARYIFKRLKFLGNKELSQGLSLLFLA 371	266 FWFRCMYMLIWGKFVLYKYVTCWLVTEGVCILTGLGFNGFEEKGKAKWDACANMKVWLFE 325 	208 YMKLVQ-GELIDIPGK-IPNSIIPALKRLSLGLFYLVGYTLLSPHITEDYLLTEDYDNHP 265 	170 SSEQQKYAIRGVPSLLEVAGFSYFYGAFLVGPQFSMNH 207	116 TTFCFQMAYLLAGYYYTATGNYDIKWTMPHCYLTLKLIGLAVDYFDGGKDQNSL 169	61YLFYKETYLIHLFHTFTGLSIAYFNFGNQLYHSLLCIVLQFLILRLMGRTITAVL 115 	11 TVVALAGVLQSGFQELSLNKLATSLGASEQALRLIISIFLGYPFALFYRH 60  :::  :::   :::  :::	A.5%; Score 116.5; DB 2; Length 736; Local Similarity 21.0%; Pred. No. 0.22; Los 108; Conservative 69; Mismatches 173; Indels 165; Gaps 27;	35 QM 31 AY 31 AY 38 AF 73 LG 73 LG 73 LG 73 LG 73 LG 73 LG 73 LG 74 LG 75 LG 77 LG 78	CAMBE HANNITA ABOATA AND AT A BELIEVE AND A SECOND COMMENT OF THE

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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Fitle: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
probable membrane protein YPL189w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein P2201
C;Species: Saccharomyces cerevisiae
C;Date: 10-Dec-1994 #sequence_revision 31-May-1996 #text_change 19-Apr-2002
C;Accession: S65208; S65201
R;Rieger, M.; Mueller-Auer, S.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S65202
A;Accession: S65208
A;Accession: S65208
A;Accession: S65208
A;Accession: S65208
A;Rotecule type: DNA
A;Rosidues: 1-609 <RIE>
A;Cross-references: EMBL:Z73545; NID:g1370394; PID:e246916; PID:g1370395; MI
A;Experimental source: strain S288C (AB972)
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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Best Local S
Matches 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: B96610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 VKLDMPQNTLSFKDVAWYGVRWLFSFLLIELMTHLFYYNAFVISGLW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 --- GKDQNSLS-SEQQKYAIRGVPS--LLEVAGFSYFYGAFLVGPQFSMNHYMKLVQGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 LTTFCFQMAYLLA----GYYYTATGNYDIKWTMPHCVLTLKLIGLAVDYFDG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  426 TIHWLFMGYSMTAFCLFTWDKWLKVYKSIYFLGHIFF 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 -----HASF----NRWLIRYMYIPLGGSRRKFLNVWVVFTFVAMWHDLEWKLLSWAWLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 ILSEVFAVFTVIANGVRSFFHLRAKGMAILWLSMSLIYLIYLHGACVIYILSIATANFLL
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4.5%; Score 115; DB
Similarity 19.4%; Pred. No. 0.14;
77; Conservative 52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C--FQMEFLIVIVERQAAR------LIQESPTLSKLAAITVLQ----PFYYLVQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLFFMPEMLL----KSASSAYKVESAFGEFLLRELKALSGAVTITCLMIANLAGYVIGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRFTGTIASFNINTNAWVARYIFKRLKFLGNKELSQGLSLLFLALWHGLH-----SGYLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKFLLLWRYFRFWSLVNGIETVENMPNCINNCYSLELF-----W-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKF-VLYKYVTCWLVTEGV------CILTGLGFNGFEEKGKAKWDACANMKVWLFETN
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                                   PID:g1370395; MIPS:YPL189w
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F;164-180/Domain: transmembrane #status predicted <TM2>
F;201-217/Domain: transmembrane #status predicted <TM3>
F;201-217/Domain: transmembrane #status predicted <TM3>
F;308-344/Domain: transmembrane #status predicted <TM4>
F;376-392/Domain: transmembrane #status predicted <TM5>
F;406-422/Domain: transmembrane #status predicted <TM7>
F;406-422/Domain: transmembrane #status predicted <TM8>
F;498-514/Domain: transmembrane #status predicted <TM8>
F;498-514/Domain: transmembrane #status predicted <TM8>
F;534-550/Domain: transmembrane #status predicted <TM9>
F;578-594/Domain: transmembrane #status predicted <TM10>
                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Buchnera
C;Date: 02-Mar-2001
C;Accession: B84949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
B84949
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A;Cross-references: SGD:S0006110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z73545; MIPS:YPL189w A;Experimental source: strain S288C (AB972) C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 177-609 <BEN>
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A; Accession: S65201
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                                                                                                A;Gene: nuoL; BU164
C;Superfamily: NADH dehydrogenaa
C;Keywords: NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;79-95/Domain: transmembrane #status
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                                                                                                                                                                      A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                      A;Residues: 1-614 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
                                                                                                                                                                                                                                                                    A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                           A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera A;Reference number: A84930; MUID:20445173; PMID:10993077
                                                                                                                                                                                                                                                                                                                                                                                           R;Shigenobu, S.; Watanal
Nature 407, 81-86, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NADH2 dehydrogenase
                                                                                                                                                                                                                                                                                                                      A; Accession: B84949
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Best Local S
Matches 56
Query Match
Best Local S
Matches 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 FDGGKDQNSLSSEQQKYAIRGVP--SLLEVAGFSYFYGAFLVGPQFSMNHYMKLVQGELI
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  l Similarity
94; Conserv
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                                                                                                                      NADH dehydrogenase
4.4%; ilarity 20.9%; Conservative
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Score 114; DB 2; Length 614;
Pred. No. 0.28;
6; Mismatches 165; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 114.5; DI
Pred. No. 0.25;
                                                                                                                      (ubiquinone)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-Mar-2001
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66;

Indels 124;

Gaps

20;

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Query Match Best Local Similarity 19.2%; Pred. No. 0.27 Best Local Similarity 19.2%; Pred. No. 0.27 Matches 95; Conservative 113; Mismatches  Qy 62 LFYKETYLIHLFHTETGLSIAYFNPGNQLYHSLL	T 15  7  7  7  7  7  7  7  7  7  7  7  7  7	Qy 26 LSLNKLATSLGASEQALRLIISIFLGYPE 68 LSINEFKIDFGFFLDGLSLSMLFVITGVGLLI Qy 83 YFNFGNQLYHSLLCIVLQFLILRLMGRTITAV Qy 143 MPHCVLTSVLVLADNFLFMYLGMEGVSV- Qy 143 MPHCVLTKLIGLAVDYFDGGKDQNSI 168 FKAFILTRVSDVFLMIGMFLIYREFNSF Qy 198 LVGPQPSMNHYMKLVQGELIDIPGKIPNSIIP Db 216DYITLFLLLGVIGKSAQLF Qy 258 TEDYDNHPFWFRCMYMLIWGKFVLYKYVTCWL
#1.4* Score 113.5; DB 2; Length 547;  milarity 19.2%; Pred. No. 0.27;  Conservative 113; Mismatches 184; Indels 103; Gaps 26;  FYKETYLIHLEHTFTGLSIAYENFGNQLYHSLLCIVLQFLILRLMGRTITAVLTTF 118	orhabditis elegans ion 29-Oct-1999 #text_change July 1998 legans cosmid ZC190. rom GB/EMBL/DDBJ PIDN:AAC26966.1; GSPDB:GN0002 ol N2; clone ZC190	

487 LPITHAMYVEKKEKI 483 	49	8 8
440 MTQAIIPVACIAFLİHFTFVIVVMLLSTLENSRYYQMTFSHYFENITSVFTICVPFL 496	44	문
423 VQQTIHWLEMGYSMTAFCLETWDKWLKVYKSIYFLGHIFFLSLEI 468	42:	S
380 YAQIIHLVDFHVIAITIMNLVDMSALVILIISSQYSIQNYRKTAGIASLEKRFQISDVYI 439	. 38	밁
384 FQMEFLIVIVERQAARLIQESPTLSKLAAITVLQPFYYL.422	38,	Ş
320 LHEFAFALHSFSIQMFSLDSKHTLKLLERYITAKQTITQSVRNQVLSITLGVIISILSMC 379	32	В
327 NPRFTGTIASENINTNAWVARYIFKRLKFLGNKELSQGLSLLFLALMHGLHSGYL-VC 383		5
266 IHAKAQSPELLLESISLEFELALTH-GEQIFELLIGADAENAIDYTSSMRLYVWSL 319	26	B
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e proteome.	nd the EMBL outstation of the EMBL outstation its restrictions on its content is in no way by and for commercial www.isb-sib.ch/announce/	; E	und A.K., Eriksson AS., N.A., Andersson S.G.E.; ndosymbiotic bacteria."; rom NADH, via FMN and iron- n the respiratory chain. translocation (for every two ions are translocated across conserves the redox energy in	5) (NADH dehydrogenase ). Enterobacteriales;		079225 puffinus na p34852 anopheles g Q94wq8 buteo buteo Q57863 methanococc Q36319 alectoris r Q33889 balearica r p35075 coturnix co Q34607 grus nigric Q79216 pachyptila p34868 galeocerdo p90396 bos taurus Q9zkw7 helicobacte

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                                                                                                                                                                                                                                                                                                                                               LVGGASLVSFPLITSGFYSKGNILFSVLKDGYFNLF----LIGLFCSF--LTSIYTFRM
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           bacterium).
Proteobacteria; Gammaproteobacteria;
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Pred. No. 0.14;
57; Mismatches 1
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                                                                        on update)
(EC 1.6.99.5)
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             Enterobacteriales;
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                                                                        (NADH dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
                                                                                                                                                                                                                                            SEQUENCE
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TRANSMEM 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00662; oxidored_q1_N; PRINTS; PR01434; NADHDHGNASE5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 407:81-86(2000).
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K, L, M, N CONSTITUTE THE MEMBRANE SECTOR OF THE COMPLEX (BY SIMILARITY).
SUBCELULIAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: TO POLYPEPTIDE 5 OF THE NADH-UBIQUINOL OXIDOREDUCTASE OF CHLOROPLASTS OR MITOCHONDRIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a proton gradient (By similarity).

CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.
SUBUNIT: COMPOSED OF 13 DIFFERENT SUBUNITS. SUBUNITS NUOA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: NDH-1 shuttles electrons from NADH, via FMN and ironsulfur (Fe-S) centers, to quinones in the respiratory chain. Couples the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are translocated across
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the cytoplasmic membrane),
                           168
 198 LVGPQFSMNHYMKLVQGELIDIPGKIPNSIIPALKRLSLGLFYLVGYTLLSPHITEDYLL
                                                                                                         83
                                                                                                                                   89
                                                                                                                                                                                        94;
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p; IPR001750; Oxidored_q1.
p; IPR001516; Oxidored_q1_N.
pridored_q1; 1.
                                                                                                                                                                                                    Similarity
                           FKAFILTRVSDVFLMIGMFLIY----REFNSFNFQEIKF----LSSFLNVENFYYL----
                                                                                                       YFNFGNQLYHSLLCIVLQFLILRLMGRTITAVLTTFCFQMAYLLAGYYYTATGNYDIKWT
                                                                                                                                   LSINEFKIDFGFFLDGLSLSMLFVITGVGLLIHIFSSWYMRYKEGQ--SRFFAYTNLFIA
                                                                                                                                                            LSLNKLATSLGASEQAL---RLIISIFLGYPFALFYRHYLFYKETYLIHLFHTFTGLSIA
                                                   MPHCVLT-----LKLIGLAVDYFDGGKDQNSLSSEQQKYAIRGVPSLLEVAGFSYFYGAF
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Pred. No. 0.44
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                                                                              -CSYLLIGFYYTELKNN--LCA
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RA Wood V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Qiver K., O'Nell S., Pearson D., Quail M.A., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Weltjens I., Vonstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Cerrittti I., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Chillard D., James J., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
"The genome sequence of Schizosaccharomyces pombe.";

RT Nature 415:871-880 (2002).
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Q09758; Q9C0
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C24H6.01c in chromosome
SPAC24H6.01C OR SPAPB21F2.01.
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                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21848401; PubMed=11859360;
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                       modified
                     European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: TO YEAST YGL084C.
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noved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce)
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                 There are no restrictions in as its content is in ved. Usage by and for com
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OCCUPATION NO OC

Cytochrome b.
MTCYB OR COB OR
Garrodia nereis

CYTB. (Grey-backed

Mitochondrion

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

storm petrel)

CYB GARNE 079203; 16-OCT-2001 16-OCT-2001 15-SEP-2003

(Rel. 40, Created) (Rel. 40, Last seq (Rel. 42, Last ann

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STANDARD;

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AL590562; CAC3689
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53 ctein;
120 1;
160 1;
192 2;
301 2;
374
445
                                               FLTLKGKKFIYF
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                                                                   DKWLKVYKSIYF
                                                                                         PILPERLCCFMSRRTGLTKHPYYRYISGFGAALNIYFMIICNLIGFAVGIDGIKNVLVSF
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                                                                                                                                     --WHRSFNRWLIRYIYVPLGGSNHSILNLFIIFTFVALWHDISWELFAWGWLI-----VL
                                                                                                                                                         ASFNINTNAWVARYIFKRLKFLGNKELSQGLSLLFLALWHGLH-----SGYLVCFQMEFL
                                                                                                                                                                                 RLFRLWSLIDDIEPPENIVRCMCNNYSAVGF-----
                                                                                                                                                                                                     KYVTCWLVTEGV------CILTGLGFNGFEEKGKAKWDACANMKVWLFETNPRFTGTI
                                                                                                                                                                                                                                               YLVGYTLLSPHITEDYLLTEDY-------DNHPFWFRCMYMLIWGKFVL-Y
                                                                                                                                                                                                                                                                       EDYNLKNFLTYIFYAPLYLAGPIISFNNFMSQM------KYPT--VSTLKYRNL---
                                                                                                                                                                                                                                                                                                                 LB-RWYVLFNITMLRLVSFNMDYYWSLKHNSEKLNTLIFDKDREPTTLTFRERVDYSCLD
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                                                                                                                                                                                                                                                                                                                                                                                                                              ASEQALRLIISIFLGYPFALFYRHYLFYKET----YLIHLFHTFTGLSIAYFNFGNQLYH
                                                                                                                                                                                                                           -LYAIRFLVCVLTMEFLLHYAYVTAISKDGNWNQYSAVESAMISFIVLFM-TWLKLLIPW
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588 AA;
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16.9%;
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3 POTENTIAL
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SER-RICH.
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Pred. No. 0.
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POTENTIAL.
POTENTIAL.
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POTENTIAL.
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).98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    198;
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Query Match
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SEQUENCE
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METAL
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MEDLINE=99003708; PubMed=9787440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Electron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR005798; Cytb_b6_C.
InterPro; IPR005797; Cytb_b6_N.
Pfam; PF00032; cytochrome_b_C; 1.
Pfam; PF00033; cytochrome_b_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF076056; AAC68613.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Body size effects and rates of cytochrome-b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: The main subunits of complex b-c1 are: cytochrome cytochrome c1 and the Rieske protein (By similarity). SIMILARITY: Belongs to the cytochrome b family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coupled to ATP synthesis (by similarity).

COFACTOR: Binds two heme groups non-covalently. Heme
b562) is low-potential and absorbs at about 562, and
or b566) is high-potential and absorbs at about 566 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00192; CYTOCHRŌMĒ B HEME; 1.
PS00193; CYTOCHROME B QO; 1.
transport; Mitochondrīon; Respiratory
                                                                                                                                                                                                                                                                                                                                                                                            MAPHIRKSHPILKMINNSLIDLP--TPSNISAWWNFGSLIGLCLVTQILTG-LLLATHYT
                                                                                                                                                                                                                                                                                                                                                                                                                                   VGPQFSMNH-YMKLVQGELIDIPGKIPNSI----IPALKRLSLGLFYLVGYTLLSPHIT
PANPLVTPPHIKPEW----
                                                                             TFLHESGSNNPLGLVSNCDKIPFHPYFSLKDTLGFMFMLFLLTTLALFSPNLLGDPENFT
                                                                                                                RLIQESPTLSKLAAITVLQ--PF--YYLVQQTIHWLFMGYSMTAFCLFTWD------
                                                                                                                                                                                            INTNAWVARYIFKRLKFLGNKELSQGLSLLFLALWHGLHSGYLVCFQMEFLIVIVERQAA
                                                                                                                                                                                                                                     --NTGILLLITLMATAFVGY----VLPW----GQMSFWGATVITNLFSAIPYIGQTIVEW-
                                                                                                                                                                                                                                                                          LVTEGVCILTGL---GFNGFEEKGKAKWDACANMKVW-----LFETNPRFTGTIASFN
                                                                                                                                                                                                                                                                                                                   ADTTLAFSSVTHTCRNVQYGWLIRNLHANGASFFFICIYLHIGRGLYYGS---YLYKETW
                                                                                                                                                                                                                                                                                                                                                       EDYLLTEDYDNH-------PFWFRCMYM-----LIWGKFVLYKYVTCW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRON 1 (HEME B562 /
IRON 2 (HEME B566 /
IRON 1 (HEME B562 /
IRON 2 (HEME B566 /

    YFLFAYAILRSIPNKLGGVLALAASVLILFLSPLLHKS

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56 AXIAL LIGAND).
72 AXIAL LIGAND).
73 6 AXIAL LIGAND).
74 BF CRC64;
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                                    LGHIFFLS----LLFILPYIHKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 380;
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                                                                                                                                                         ------LPFMIAGLTLIHL
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MBL outstation -
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079218;
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InterPro; IPR005798; Cytb b6 C.
InterPro; IPR005797; Cytb b6 N.
Pfam; PF00032; cytochrome b C; 1.
Pfam; PF00033; cytochrome b N; 1.
PF00033; cytochrome b N; 1.
PROSITE; P800192; CYTOCHROME B HEME; 1.
PROSITE; P800193; CYTOCHROME B OO; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
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Pelecanoides garnoti
                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytochrome
                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nunn G.B., Stanley S.E.; "Body size effects and rates of cytochrome-b evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99003708; PubMed=9787440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Isolate PDP-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pelecanoides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitochondrion.
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seabirds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).

SUBUNIT: The main subunits of complex b-cl are: cytochrome cytochrome cl and the Rieske protein (By similarity).

SIMILARITY: Belongs to the cytochrome b family.
                                                                                                                                                                                                                                                                                                                                                                                                                                   European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity). COPACTOR: Binds two heme groups non-covalently. Heme 1 (or BL b562) is low-potential and absorbs at about 562, and heme 2 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PELGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Evol. 15:1360-1371(1998).
FUNCTION: Component of the ubiquinol-cytochrome c complex (complex III or cytochrome b-cl complex),
                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                   247
                                                                                                        199
 283
                         52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           b566)
                                                                                                                               . Similarity
75; Conserv
                                                                                                     VGPQFSMNH-YMKLVQGELIDIPGKIPNSI-----IPALKRLSLGLFYLVGYTL
 KYVTCWLVTEGVCILTGL---GFNGFEEKGKAKWDACANMKVW----
                                                   LSPHITEDYLLTEDYDNH
                                                                             MAPNLRKSHPLLKMVNNSLIDLP--VPSNISAWWNFGSLLTICLLTQILTGL-----L
                         LAMHYTADTTLAFSSVAHTCRNVQYGWLIRNLHANGASFFFICIYLHIGRGLYYGS---Y
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                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is high-potential and absorbs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40, Created)
40, Last sequence up
42, Last annotation
                                                                                                                                                                                                84
98
183
197
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Neognathae; Procellariiformes; Pelecanoididae;
                                                                                                                                                                                   42653
                                                                                                                                           20.5%;
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                                                                                                                                                                                   MW.
                                                                                                                                 47;
                                                                                                                                                                                               IRON 2
IRON 1
IRON 2
                                                                                                                                           Pred.
                                                                                                                                             Score 107;
Pred. No. 0.
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                                                                                                                                 Mismatches
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(HEME B566 AXIAL LIGAND)
(HEME B562 AXIAL LIGAND)
(HEME B566 AXIAL LIGAND)
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.MBL;
£MBL; AE00050.

PIR; A65086; A65080.

PIR; A65086; E611800; hybb.

EcoGene; E611800; hybb.
InterPro; IPR005614; NrfD; 1.

Pfam; PP03916; NrfD; 1.

Pfam; PP03916; NrfD; 1.

Transmembrane; Electron transport; Heme; Companies and potential.

12
32
POTENTIAL.
                                                                                                                                                              EMBE; U09177; AAA21590.1; -- EMBE; U28377; AAA69162.1; ALT_SEQ. EMBE; AE000382; AAC76031.1; -- PIR) A65086; A65086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
-!- FUNCTION: PROBABLE B-TYPE CYTOCHROME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=K12 / TG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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HYBB OR B2995.
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16-OCT-2001
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01-OCT-1994
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(Rel. 40, Last annotation update)
/Fe-hydrogenase 2 B-type cytochrom
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                                                                                  Complete proteome.
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PILP
                             FILP
                                                                                     LQPFYYLVQQTIHWLFMGYSMTAF-----CLF-TWDKWLKV--YKSIYFLGHIFFLSLL
                                                                                                                   ELIYRDKLSLAFAG-----DFYSVMFWIEVLLMLFPLVVLRVANVRNDSRMLFLSALSA
                                                                                                                                                                               AGLRGNGPDEKS------LF---VKLTNTIS-----VLLAIFIVLRF-G
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                                                         L-----LGCATWR-LTYSLVAFNPGGGYAYFPTWEELLISIGFVAIEICAYIVLIRLL
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059831;
16-OCT-2001
16-OCT-2001
28-FEB-2003
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A. Sgource J., Peat N., Hayles J., Bakham D., Bowman S., Barooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.
                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Putative amino-acid permease C965.llc.
                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                              Schizosaccharomycetales; Schizosaccharomyces.
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                                                                                                                                                                     MEDLINE=21848401; PubMed=11859360;
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Stewart A.,

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RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Oliver K., O'Neil S., Pearson D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rabiton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gablel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Domainguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
"The genome sequence of Schizosaccharomyces pombe.";
"The genome sequence of Schizosaccharomyces pombe.";
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Best Local
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SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: Belongs to the amino acid permease family.
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                                                                                                                                                                                                                                                                                           FYKETYLIHLFHTFTGLSIAY------FNFGNQLYHSLLCIVLQFLILRLMGRTIT 112
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                                                   I-MNYSTG----
                                                                                                  LAVDYFDGGKDQNSLSSEQQKYAIRGVPSLLEVAGFSYFYGAFLVGPQFSMNHYM----K
                                                                                                                                                        AVILITC--LSSINSGIYIGSRSLYNLAKDGMAPKIFKRVDKRGVPWVAVHSVHLFGFLS
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Mismatches 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytochrome c oxidase polypeptide I (EC 1.9.3.1).
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                                                                          METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Locusta migratoria (Migratory locust).
                                                                                                                                                                 Oxidoreductase; Heme; Copper; Mitochondrion; Transmembrane;
                                                                                                                                                                                                                                HSSP; P00396; 20CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence, organization, and evolution of the Locusta migratoria
                                                                                                                                                                                            PRINTS; PR01165; CYCOXIDASEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .5-JUL-1999
                                                                                                                                                                                ROSITE; PS00077;
                                                                                                                                                                                                                    interPro; IPR000883; COX1.
                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: Respiratory chain; terminal step.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE. CONTAINS 12 POTENTIAL TRANSMEMBRANE DOMAINS.
SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
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38, Last sequence update)
42, Last annotation updat
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                                      MW.
Score 106; DB Pred. No. 1.4;
                                                COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
IRON (HEME A3 AXIAL LIGAND) (PROBABLE).
IRON (HEME A AXIAL LIGAND) (PROBABLE).
1'-histidyl-3'-tyrosine (By similarity)
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079224;
                     This
                                                                                                                                                                                                                              Archosauria, Aves, Chordata, Craniata, Vertebrata, Euteleostomi, Procellariinae, Pterodroma.

NCBI_TaxID=79640;
                                                                                                                                                                                          STRAIN=Isolate Bonin-1;
MEDLINE=99003708; PubMed=9787440;
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     Pterodroma hypoleuca (Bonin
                                                                                                                                                                                                                                                                                                MTCYB OR COB OR CYTB.
                                                                                                                                                                                                                                                                                                             Cytochrome
                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
15-SEP-2003 (Rel. 42,
                                                                                                                                                                        "Body size effects and rates of cytochrome-b
                                                                          FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-cl complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL 562) is low-potential and absorbs at about 562, and heme 2 (b-corpose) is high-potential and absorbs at about 566 (By
                                     SUBUNIT: The main subunits of complex b-c1 are: cytochrome c1 and the Rieske protein (By simila: SIMILARITY: Belongs to the cytochrome b family.
  European
                                                                      similarity)
                                                                                                                                                    Biol. Evol. 15:1360-1371(1998).
                                                                                                                                                                                    G.B., Stanley
         SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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Crozier R.H., Crozier Y.C., Mackinlay A.G.;
"The CO-I and CO-II region of honeybee mitochondrial DNA: erfor variation in insect mitochondrial evolutionary rates.";
Mol. Biol. Evol. 6:399-411(1989).
                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda;
Neoptera; Endopterygota; Hymeno;
Apidae; Apis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as lone modified and this statement is not remove entitles requires a license agreement (so or send an email to license@isb-sib.ch).
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InterPro; IPR005797; Cytb b6 N.
Pfam; PF00032; cytochrome b C;
Pfam; PF00033; cytochrome b N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF076079; AAC68636.1;
                                                                                               MEDLINE=90136028; PubMed=2559293
                                                                                                                                                                                                                                                                            Apis mellifera ligustica (Common
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(Rel. 17, Last sequence update)
(Rel. 42, Last annotation update)
c oxidase polypeptide I (EC 1.9.3.1).
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Pred. No. 1.
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  (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence and genome organization.";

Genetics 13:97-117(1933).

-i- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATION THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT OF THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBUNIT OF THE ENZYME ELECTRONS ORTGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Thorax;
MEDLINE=93114603; PubMed=8417993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M23409; AAA18476.1; -.
EMBL; LO6178; AAB96799.1; -.
PIR; A32431; A32431
HSSP; P18401; 1FFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The mitochondrial genome of the honeybee Apis mellifera: complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Respiratory
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase; Heme; Copper; Mitochondrion; Transmembrane;
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PROSITE; PS00077; COX1; 1.
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PATHMAY: Respiratory chain; terminal step.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL

INNER MEMBRANE. CONTAINS 12 POTENTIAL TRANSMEMBRANE DOMAINS.

INNER MEMBRANE. TO THE HEME-COPPER RESPIRATORY OXIDASE FAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
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CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 254
                                                               197
                                                                                              238
                                                                                                                              147
                                                                                                                                                             185
                                                                                                                                                                                                                             141
                              284 YVTCWLVTEG------VCILTGLGFNGFEEKGKAKWDACANMKVWL------
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                                                                                                                                                                                                                                                                                        88 NQLYHSLLCIVLQFLILRLMGRTITAVLTTFCFQMAYLLAGYYYTATGNYDIK-----
                                                                                                                                                                                                                                                                                                                           93;
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                                                                                                                            SLHMSGISSIMGSLNLMVTIMMMKNFSMNY------DQISLFPWSVFITAILLIMS
                                                                                                                                                                                          MAFPRMNNISFWLLPPSLFMLLLSNL---FYPSPGTGWTVYPPLSAYLYHSSPSVDFAIF 146
                                                                                                                                                                                                                        -----WTMPHCVLTLKLIGLAVDYFDGGKDQNSLSSEQQKYAIRGVPSL----
                                                                                                                                                                                                                                                            DQIYNTIV-----GNWLIPLMLGSPD
                                                            LPVLAGAITML---LFDRNFNTSFFDPMGGGDPILYQHLFWFFGHPEVYILILPGFGLIS
                                                                                            LFYLVG-YTLLSPHITEDYLLTEDYD-----NHPFWF---RCMYMLIWGKFVLYK
                                                                                                                                                          -LEVAGESYFYGA-----FLVGPQFSMNHYMKLVQGELIDIPGKIPNSIIPALKRLSLG
                                                                                                                                                                                                                                                                                                                                                                                        521 AA;
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242
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COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
                                                                                                                                                                                                                                                                                                                      Score 105; DB 1;
Pred. No. 1.7;
1; Mismatches 148
                                                                                                                                                                                                                                                                                                                                                                                                    IRON (HEME A3 AXIAL LIGAND)
IRON (HEME A AXIAL LIGAND)
1'-histidyl-3'-tyrosine (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRON (HEME A AXIAL LIGAND) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                        2149417AC981CE64 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROBABLE).
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                                                                                                                                                                                                                                                                                                                           148;
                                                                                                                                                                                                                                                                                                                                                      Length 521;
                                                                                                                                                                                                                                                                                                                        Indels
- IVWAHHMFTVGLD
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                                                                                                                                                                                                                                                                                                                                                                                                       similarity)
                                                                                                                                                                                                                                                                                                                      178;
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SUBUNITS 1-
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                                                              253
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WIMPHCVLTLKLIGLAVDYFDGGKDQNSLSSEQQKYAIRGVPSLLEVAGFSYFYGA 19	Ş
342 VSSFYSKHIILEKMLDMNCNFFTSMMFMLGTLLTGMYSIRLMKFLCWGNNNNKFSYCNMS 401	Db
112 TA	8
	Db .
61 YLFYKETYLIHLFHTFTGLSIAYFNFGNQLYHSLLCI-VLQFLILRLMGRTI 111	Ş
4 SAEGDEGTVVALAGVLQSGFQELSLNKLATSLGASEQALRLIISIFLGYPF-ALFYRH 60	B 8
Query Match 4.1%; Score 105; DB 1; Length 545; Best Local Similarity 24.0%; Pred. No. 1.8; Matches 81; Conservative 42; Mismatches 128; Indels 86; Gaps 1	Ma Be
KINTS; PR01434; NADHDHGNASE5. idoreductase; NAD; Ubiquinone RQUENCE 545 AA; 61335 MW;	SQ KW
terPro; IPR am; PF00361 am; PF00662	무무무
IBL; X83390; CAA58296.1; IR; S59143; S59146; NADHub terPro; TPR003916; NADHub	
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se by non-profit institutions as long as its content is in no diffied and this statement is not removed. Usage by and for commerc this in the statement is not removed.	888
ais SWISS-PROT entry is copyright. It is produced through a collab tween the Swiss Institute of Bioinformatics and the EMBL outst be Buronean Bioinformatics Institute There are no restrictions	388
netics 140:1353-1366 (1995) CATALYTIC ACTIVITY: NADH + ubiquinone = NAD	388
omplete sequence and gene the land snail Albinaria	RRR
EQUENCE FROM N.A. EDLINE=96120351; PubMed=74	RRR
	2000 2000 2000 2000 2000 2000 2000 200
Albinaria coerulea (Land snail). Mitochondrion.	8 8 8
01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 01-FEB-1996 (Rel. 33, Last annotation update) NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).	
JUT 11 1 ALBCO 1 NUSM ALBCO STANDARD; PRT; 545 AA. P48918;	RES NU5 AC
389 SSFIHWYPLITGLLLNIKWLKIQFIMMFIGVNLTFFFQHFLGLMSMFRR 437	D
424 QQTIHWLEMGYSMTAFCLETWDKWLKVYKSIYELGHIFELSLLEILPYIHKAM-VPRK 480	8
342 FIMLFTIGGLTGIMLSNSSIDIILHDTYYVVGHFHYVLSMGAVFAII 388	Дb
380 YLVCFOMEFLIVIVERQAARLIQESPTLSKLAAITVLQPFYYLV 423	Ş
297 VDTRAYFTSATMIAVPTGIKVFSWLATYHGSKLKLNISILWSLG 341	뭣
INTRETGITASENININAWVARILEN	Ş

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329 557

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RESULT 12
NU5M_RHIST
                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institute. There are no restrictions modified and this statement is not removed. Usage by and for commentities requires a license agreement (See http://www.i-t-torsend an email to licensesia.
                                                                                                                                                                                                                                                                                                                                               Pfam; PF00361; oxidored_q1; 1.
Pfam; PF00662; oxidored_q1 N; 1.
PRINTS; PR01434; NADHDHGNASE5:
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE .654 AA; 72818 MW; 22D2E025B8D6E12E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paquin B., Roewer I., Wang Z., Le
"A robust fungal phylogeny using
protein sequence.";
Can., J. Bot. 73:S180-S185(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; | T14202; T14202.
InterPro; IPR003916; NADHub_oxred5.
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STRAIN-DAOM 148428;
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01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.
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01-0CT-1996
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InterPro; IPR001516; Oxidored_q1_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
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                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                     87;
                                                                                                                                                                                                                                                                                                         Similarity
                   APLIMATP-LVVLAVFSTFFGYVTKDLFVGMGTDFYNNALFIHPNHSI--
                                                                                                                                                  GSVIHAMNDEQDLRKFGGLSRLLPFTYSMMVIGSLSLMALPFL-TGFYSKDLIIELAYGH
                                                                                                                                                                                    TYLIHLEH-----TFTGLS-IAYENEGNQLYHSLLCIVLQELILRLMGRTITAVLT---
                                                                                                                                                                                                                                                    ALAGVLQSGFQELSLNKLATSLGASEQALRLIISIFLGYPFALF-----YRHYLFYKE
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                                                KYAIRGVPSLLEVAGFSYFYG------AFLVGPQFSMNHYMKLVQGELI
                                                                                   YSFSGNLVYWLASVAAVFTAMYSIR----SLYLTFLG--
                                                                                                                                                                                                                   ATTGLLONDLKRVIAYSTCSQLG-----LLFLVCGLSQYNVALFHLVNHAWFKALLFLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FYPTLMSSMMFLGPTSYNLLHYTKSLLIYMKRIDLSISEPNWVMSNLMYSSSWRVMSLFN
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                                                                                                                   -TFCFQMAYLLAGYYYTATGNYDIKWTMPHCVLTLKLIGLAVDYFDGGK-DQNSLSSEQQ
                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zygomycota;
                                                                                                                                                                                                                                                                                                     4.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rhizopus nigricans)
                                                                                                                                                                                                                                                                                     59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z., Lang B.F.;
using the mitochondrially encoded
                                                                                                                                                                                                                                                                                  Score 105; DB 1; L
Pred. No. 2.1;
9; Mismatches 164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                      22D2E025B8D6E12D CRC64;
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                                                                              EMBL; Y16474; CAA76246.1; -.
EMBL; Y09849; CAA70979.1; -.
PIR; A71390; A71390;
InterPro; IPR005798; Cytb_b6_C.
InterPro; IPR005797; Cytb_b6_N.
Pfam; PF00032; cytochrome_b_C; 1.
Pfam; PF00033; cytochrome_b_N; 1.
PROSITE; PS00192; CYTOCHROME_B_RO; 1.
PROSITE; PS00193; CYTOCHROME_B_BOO; 1.
Electron transport; Mitochondrion; Resp
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P92472; O79415;
15-JUL-1998 (Rel. 3
15-DEC-1998 (Rel. 3
15-SEP-2003 (Rel. 4
                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 Heme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spruyt N., Delarbre C., Gachelin G., Laudet V.; "Complete sequence of the amphioxus (Branchiostoma mitochondrial genome: relations to vertebrates."; Nucleic Acids Res. 26:3279-3285(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
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MTCYB OR COB OR CYTB
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                                                                                                                                                                                                                                                                                                                                                                                                                                            respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity). Heme 1 (or BL 5562) is low-potential and absorbs at about 562, and heme 2 (or similarity).
                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: The main subunits of complex b-c1 are: cytochrome cytochrome c1 and the Rieske protein (By similarity). SIMILARITY: Belongs to the cytochrome b family.
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 84
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RESULT 14
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                 STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connertton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Fritz C., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            Presecan E., Santana M., Schneider E., Sch
Rapoport G., Danchin A.;
"Bacillus subtilis genome project: cloning
kb region from 325 degrees to 333 degrees.
Mol. Microbiol. 10:371-384 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glaser P., Kunst F., Arnaud M., Coud
Hullo M.F., Ionescu M., Lubochinsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis.
Bacteria; Firmicutes;
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DLTB OR IPA-4R.
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01-FEB-1995
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95020537; PubMed=7934828;
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K., Haiech J.,
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A Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
A Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
A Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
A Medina N., Mellado R.P., Miuno M., Moestl D., Nakai S., Noback M.,
A Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
A Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
A Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
A Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
A Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
A Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.
A Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
A Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
A Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo
A Sarokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
A Sorokin A., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
A Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
A Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
A Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
A Viari A., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
A Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
The complete genome sequence of the Gram-positive bacterium Bacill
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Incorporation of D-alanine into lipoteichoic acid acid in Bacillus subtilis. Identification of genes J. Biol. Chem. 270:15598-15606(1995).
                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
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Kobayashi Y., Koetter P., Koningstein
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PATHWAY: D-Alanyl-lipoteichoic acid biosynthesis.

SUBCELLULAR LOCATION: Integral membrane protein (Potentia
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PF03062; MBOAT; 1
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                                CLFTIWQVLLISGYLAYRQKANSGFVFCGAVIASILPLFLSKIWPFLSHPQPHHPPHNLI
----CVLTLKLIGLAVDYFDGGKDQNSLSSEQQKYAIRGVPSLLEVAGFSYFYGAFLVG
                                                                   TTFCFQMAYLLAGYY-YTATGNYD
                                                                                                                                      YRHYLFYKETYLIHLFHTFTGLSIAYFNFGNQLYHSLLCIVLQFLILR--LMGRTITAVL
                                                                                                     YSSFLFFILLGILLLPTIILGLNGKRF----QAYNMFISIIILALIFSHDLHG---VIAL
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                                                                                                                                                                       Score 104.5; I
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                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Phylogenetic relationships of the ratite birds: resolving between molecular and morphological data sets."; (In) Mindell D.P. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Lee K., Feinstein J., Cracraft J.;
InterPro; IPR005798; Cytb b6 C.
InterPro; IPR005797; Cytb b6 N.
InterPro; IPR005797; Cytb b6 N.
InterPro; IPR005797; Cytb b6 N.
Iffam; PF00032; cytochrome b C; 1.
InterPro; IPR0033; cytochrome b N; 1.
IPROSITE; PS00192; CYTOCHROME B HEME; 1.
IPROSITE; PS00193; CYTOCHROME B QO; 1.
IPROSITE B QO; PS00193; CYTOCHROME B QUE B QO; 1.
IPROSITE B QUE B 
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Archosauria; Aves; Palaeognathae; Tinamiformes; Tinamidae; Tinamus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytochrome b.
MTCYB OR COB OR CYTB
                                                                                                                                                                                                                                EMBL; U76056; AAB61330.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Avian molecular evolution and systematics, pp.1-1, New York (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complex (complex III or cytochrome b-ci complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity). COPACTOR: Binds two heme groups non-covalently. Heme 1 (or BL b562) is low-potential and absorbs at about 562, and heme 2 (or b566) is high-potential and absorbs at about 566 (By or b566) is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytochrome c1 and the Rieske protein (By similarity). SIMILARITY: Belongs to the cytochrome b family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).

SUBUNIT: The main subunits of complex b-cl are: cytochrome cytochrome cl and the Rieske protein (By similarity).
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(Rel. 36, Last sequence update)
(Rel. 42, Last annotation update)
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                                                                                                                                                        LTFLHESGSNNPLGIISQSDKIPFHPYFTTKDMLGFTLMFFPLLTLAFFFPNFLGDPENF 257
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length: 2000000000
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1: /cgm2_6/ptodata/1
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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            US-09-634-238-216
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	9, Appl	10, App	9, Appl	2, Appl	4, Appl	19, App	19, App	•	•	•		2, Appl	11, App	11, App	7942, A	6929, A	5276, A	+1004

ALIGNMENTS

#### ; LENGTH: 484 TYPE: PRT ; ORGANISM: Lactobacillus rhamnosus US-09-634-238-216 RESULT 1 US-09-634-238-216 GENERAL INFORMATION: Sequence 216, Application Patent No. 6544772 Best Local Similarity Matches 100; Conserv SOFTWARE: F APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Query Match PILE REFERENCE: 11000.1043U1 CURRENT APPLICATION NUMBER: US/09/634,238 CURRENT FILING DATE: 2000-08-08 NUMBER OF SEQ ID NOS: 422 SOFTWARE: FASTSEQ for Windows Version 4.0 TITLE OF INVENTION: Polynucleotides, materials incorporating TITLE OF INVENTION: them and methods for using them. APPLICANT: APPLICANT: APPLICANT: 260 204 148 144 WISSRGLTTLNRIGSMAGTAMFLMSILFIILAVTÄPLMVKGVHVÄTPNMGDIHTYLPKFD 105 RLMGRTIT-----AVLTTFCFQM------AYLLAGYYYTATGNY-DIKWTMPHCV 85 46 ISIFLGYPFALFYRHYLFYK-ETYLIHLFHTFTGLSIAYFNFGNQLYHSLLCIVLQFLIL LTEDYDNHPFWFRCMYMLIWGKFVLYKYVTCWLVTEGVCILTGLGFNGFEEKGKAKWDAC LAYYAAWTYWVVHIPYLAQKPQAILIALSWLFKG-NGDFVNTVSSMTVSLICLALFLLFL GMLFNSHH---GPQFSMNHYMKLVQGELIDIPGKIPNSII---PALKRLSLGLFYLVGYTLLSPHITEDYL LNYFTTISMLVFAV----GGAEKISPYVNNTKHASKEFPLGMLVLAGMVAFCALLGSFGM L----TLKLIGLAVDYFDGGKDQNSLSSEQQKYAIRGVP-SLLEVAG----FSYFYGAFLV Coolbear, Holland, Ross O'Toole, Paul W. Reid, Julian R. Lubbers, Mark W. Dekker, James Christensson, Anna C. Havukkala, Ilkka J. Bloksberg, Leonard, Glenn, Matthew Conservative 4.4%; Score 113; DB 4; Length 484; 20.4%; Pred. No. 0.0019; Live 70; Mismatches 155; Indels 1 US/09634238 z Indels 166; Gaps

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wood, John N.
APPLICANT: Akopian, Armen N.
TITLE OF INVENTION: Ion Channel
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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CITY: Wilmington
CTATE: Delaware
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hohenschutz, Liza D
REGISTRATION NUMBER: 33,7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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  LCIVVNTVFMAMEHYPMTDAFDAMLQAGNIVFTVFFTMEMAFKIIAFDPYYY-----FQK
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                                                                                                                                                                                                                                   4.1%; Score 105; DB ilarity 19.4%; Pred. No. 0.13; Conservative 74; Mismatches
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PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: LYNN DOUCETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
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                                                                             231 LKRLSLGLFYLVGYTLLSPHIT----
                                                                                                                                                                                                                                     124 YLLAGYYYTATGNYDIKWTMPHCVLTLKLIGLAVDYFDGGKDQNSLSSEQQKYAIRGVPS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289
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                                                                                                                                                        184 LLEVAGFSYFYGAFLVGPQFSMNHYMKLVQGELIDIPGKIPNSIIP------A
                                                                                                                                                                                               60 NLLGQKYLSAQ-----LFCFIIYVIWQVALIMYYYQSRQKKNTFT----KFVTIMVLS
                                                                                                                                                                                                                                                                            12 YGTFTFFLIAFI-----VLIPVIILGFLGKRSYIYNGISTAIMIVIIFASDKH
                                                                                                                                                                                                                                                                                                              73 FHTFTGLSIAYFNFGNQLYHSLLCIVLQFLILRLMGR------TITAVLTTFCFQMA 123
                                                                                                                 ILPLAIVKILQSSWLGG-----HQIHFHESKLIEFVGFLGISYVTFKSVQLIMEIRDGS
  FVLYKYVTCWLVTEGVCILTGLGFNGFEEKGKAKWDACANMKVWLF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KWNIFDCVIVTVSLLELS-----ASKKGSLS-----VLRSLRLALDTTGQKSFLSAGY 775
                                      IKEIKVG--KLIQFISFFPTISSGPIDRYKRFVKDDKKVPSGAEYRELVVKAIHMIMLG-
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                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                     4.0%; Score 102.5; D
16.0%; Pred. No. 0.02;
ative 74; Mismatches
                                                                             -EDYLLTEDYDNHPFWFRCMYMLIWGK 278
                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                       165;
                                                                                                                                                                                                                                                                                                                                                       Indels 159;
                                                                                                                                                                                                                                                                                                                                                                                         Length 412;
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US-09-328-352-7069
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US-09-328-352-7069
                                                                                                                                                                                                                                                                                              RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7069, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SEQ ID NO 7069
                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.9%;
Best Local Similarity 21.3%;
                                                                                                                                                                                                                            Sequence 29870, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT||APPLICATION NUMBER: US/09/252,991A
CURRENT||FILLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILLING DATE: 1999-02-18
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  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                          213 QGELIDIPGKIPNSIIPALKRLSLGLFYLVGYTLLSPHITEDYLLT 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 FYRHYLFYKETYL------IHLFHTFTGLSIAYFNFGNQLYHSLLCIVLQFLILRL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 TVVALA--GVLQSGF------QELSLNKLATSLGASEQA--LRLIISIFLGYPFAL
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; Pred. No. 0.047;
42; Mismatches
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Matches
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NUMBER OF SEQ ID NOS:
SEQ ID NO 29870
LENGTH: 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3878, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
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                                     TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3878:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                                                              FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: CD/RO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 7310 CORRESPONDENCE ADDRESS:
                                                                                                                              TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     457
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                                                                                                                                                   REFERENCE/DOCKET NUMBER: GT
                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/085,598
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                     ENGTH: 401 amino acids
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENOME THERAPEUTICS
                                                                                                              (781)893-5007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD/ROM IS09660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and David Bush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
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; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-8050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6562958
GENERAL INFORMATION:
                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                            SEQ ID NO 8050
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Best Local :
                                                                                                                                                                        Query Match
Best Local Similarity
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUWANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   loca1
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LOCATION: (B) LOCATION 1...401
SEQUENCE DESCRIPTION: SEQ ID NO: 3878:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 3.8%; Score 98.5; DB 4; Similarity 18.6%; Pred. No. 0.052;
                                                                                                            TVVALAGVLOSGFQELSLNKLATSLGASEQALRLIISIFLGYPFALFYRHYLFYKETYLI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRL----KFLGNKELSQGLS----LLFLALWHGLHSGYLV
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                                  HLFHTFTGLSIAYFNFGNQLYHSLLCIVLQFLILRLMGRTITAV----LTTFCFQMAYLL 126
                                                                        SLVGLAAVLIAVAAILHNNQLTALFAQNEAALT-----AAGVQHAHMSK----V 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HMIPYAEPFYFFL-----LAIA-----LVPIVLSLLIWEKRLPVYQSAVTLFF
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HLFELFVGCFVGAITFTASVF-----AYGKLAAKKWAKTISGAWVKPVQALIF-VAMLA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGFNGFEEKGKAKWDACANMKVWLFETNPRFTGTIASFNI-----NTNAWVARYIF 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGQVLL-PVVGRIAL-----QHGGISWALVGYMYVYSMYLFFDFAGYSLFAVGTSYMMG
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                                                                                                                                                        Conservative
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                                                                                                                                                                        Score 97.5; DB 4; Pred. No. 0.089;
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                                                                                                                                                    Mismatches
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RESULT 9
US-09-328-352-7176
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US-09-252-991A-32219
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                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. BRETON et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32219
LENGTH: 545
                                                            CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7176
                                                                                                                                                                                                                                                                   Sequence 7176, Application US/09328352 Patent No. 6562958
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
ORGANISM: Acinetobacter baumannii
                         TYPE: PRT
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ORGANISM: Pseudomonas
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les 62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                      -----PFSQILRRRGTWAFALAYSITAPVFWFYLYWLPPFLNQQYGLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-328-352-7176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BUMCANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7092, App
Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                          151 KLIGLAVDYFDGGKDQNSLSSEQQKYAIRGVPSLLEVAGFSYFYGAFLVGPQFSMNHYMK 210
                                                                                  206
                                                                                                                          211 LVQGELIDIPGKIPNSIIPAL-KRLSLGLFY------LVGYTLLSPHITE--
                                                                                                                                                                      183
                                                                                                                                                                                                                                                           129
                                                                                                                                                                                                                                                                                              115 LTTFCFQMAYLLAGYYYTATGNYD------150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 GFEEKGKAKWDACANMKVWLFETNPRFTGTIASFN--INTNAWVARYIFKRLKFLGNKEL
  266
                                        254 DYLLTEDYDNHPFWFRCMYMLIWGKFVLYKYVTCWLVTEGVCI 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 VSFLPWL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          468 I--LPYI 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 IVSPWLYĽVÓSKYPÓFLHYFFIDOQFNRFSSKEFNNKOPW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 VLQPFYYLVQ----QTIHWLFMGYSMTAFCLFTWDK---WLKVYKSIYFLGHIFFLSLLF 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 -FLFVKKHISENVÄQLTVIILATNLLEFGSSQYINHDLLLTSWITISVLCFVDF----TI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 LTEDYDNHPF-----WFRCMYMLIWGKFVLYKYVTCWL----VTEGVCILTGLGFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 LTPRIDGLPFMHKPPLLHWLSSMFMELFG-----VHVWVLRLVPVLAGTLMLVGL---
                                                                                                                                                                                                                                                                                                                                         71 ILGAILFIAYELCFSFALAYSKTAQQAIEVSIVNYLWPSL--TVLAFVIFRELKFNVFII 128
                                                                                                                                                                                                                                                                                                                                                                                 63 F-----YKETYLIHLFHTFTGLSIAYFNFGNQLYHSLLCIVLQFLILRLMGRTITAV 114
                                                                                                                                                                                                                                                                                                                                                                                                                             12 TLIGLSAILMWASMVGFVKHITTAIGPDVGITLIYSLSALLLLI-IFRVPNFKLISKKYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 TVVALAGVLQSGFQELSLNKLATSLGA-----SEQALRLIISIFLGYPFALFYRHYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 3.6%; Score 93; DB 4
Similarity 20.4%; Pred. No. 0.14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SARKSILFLGYIAGAAAFLSKGLIGILIPGMILLPWLIYTKQWKKIPSLLNPLAILLFLL
AMLVLQTELSISFW-QGTAMVTAGSLI-----CWLSTNWAVI
                                                                                                                                                                  KM------GKGONPIS------IFFLGV------ALTLWLK
                                                                             LLESGQVSLPSLDLNTILSLIVASAAIGLGYAAWNIGIIHGNITMLVVASYFTPIISSLL
                                                                                                                                                                                                                                                    L-----GLLISISGIIFIQTGNGDFSLGRVVDNFHSNPLSYILAFIGAIIWAF-YCVLTK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09328352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49; Mismatches 114; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96; Indels
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301
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                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617) 526-60
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vc
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,047A
FILING DATE: 24-Apr-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/044,869
FILING DATE: 25-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MURPHY, Chery
STOREY, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein SEQUENCE DESCRIPTION: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
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ADDRESSEE: HALE AND DORR LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 41
349
                                                                                                                                                                                                          136 NYDIKWTMPHCVLTLKLIGLAVDYFDGGKDQNSLSSEQQKYAIRGVPSLLEVAGFSYFYG 195
                                                                                                                                                                                                                                                                                                                                         164 SFGMLVLSLFTTKVALYVLLKFFSGESIILY-------FGIFTSIYAAIFAF
                                                                                                                                                                                                                                                                                              87 GNQLYHSLLCIV-----LQFLILRLMGRTITAVLTTFCFQMAY-LLAGYYYTA----TG
                                                                                                                                                                                                                                                                                                                                                                                   27
                                                                                                                                                                                                                                                                                                                                                                                                                         75;
                                                                                                                                                                                                                                                    LEQNVRRLMAYMFVGQAGLLMMAIGCPGIPSDLIIVQLSFSVLYQLLLGMFADSVVKRSG
                                                                                                                                                                                                                                                                                                                                                                                 SLNKLATSLGASEQALRLIISIFLGYPFALFYRHYLFYKETYLIHLFHTFTGLSIAYFNF 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Superko, Colleen REGISTRATION NUMBER: 39, REFERENCE/DOCKET NUMBER:
LKPCST----TPEYAPSPFSSKLSIIML---
                                     LSPHITEDYLLTEDYDNHPFWFRCMYMLIWGKFVLYKYVTCWLVTEGVCILTGLGFNGFE 306
                                                                                FVTKGLMLHMNLQSFDYMLLKYMQPMLGWLL-
                                                                                                                        AFLVGPQFSMN-------HYMKLVQGELIDIPGKIPNSIIPALKRLSLGLFYLVGYTL 246
                                                                                                                                                                  HVDIN-RMAGC---FKLASME-------AMGCIVALLNLGGFPWTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 506 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BELIT, Gerald A.
COUGHLIN, Richard T.
INVENTION: NUCLEIC ACIDS, PROTEINS, AND METHODS OF
USE OF GRANULOCYTIC ERHLICHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                             3.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 526-6000
                                                                                                                                                                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 93; DB 4; Length 506;
Pred. No. 0.29;
IS; Mismatches 133; Indels
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-SLIITVSGVLYGEGLLFS--E
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RESULT 12
US-09-107-532A-5141
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 5141: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: p
HYPOTHETICAL: YE
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                   LOCATION: (B) LOCATION 1...793
SEQUENCE DESCRIPTION: SEQ ID NO: 5141:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
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MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                          383
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                                                                                                                                                    12 VVALAGVLQSGFQELSLNKLATSLGASEQALRLIISIFLGYPFALFYRHYLFYKETYLIH 71
                                                                                 72
                                                                                                                IVLVSAVYFAGIMMVLLSTI-TNLSAISRLFQVLL-----PFS----FNFLDQTVNLL
                                      VGFLLLGLARALSVKVKKAFLPTIALLSFGILNTITRTLSWQLILVYVLILLAVWLSRTE
                                                                                 LFHTFTGL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: <Unknown>
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                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/107,532A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 793 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (781)893-5007
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(B) LOCATION 1...793
                                                                                                                                                                                                                      20.8%;
                                                                                                                                                                                               3.6%; Score 93; DB 4; Length 793;
20.8%; Pred. No. 0.57;
ive 47; Mismatches 115; Indels
  -ITAVLTTFCFQMAYLLAGYYY-----TATGNY-----DIKWTMP 144
                                                                             ----SIAYFNFG-----NQLYHSLLCIVLQFLILRLMGRT- 110
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AND AMINO ACID SEQUENCES RELATING
FAECIUM FOR DIAGNOSTICS AND THERAL
                                                                                                                                                                                                 82;
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                                                                                                                                                                                               Gaps
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                                                                                                                      382
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                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                    Query Match 3.6%;
Best Local Similarity 20.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC COMPS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/097,889
FILING DATE: 15-UN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Herrnstad
APPLICANT: Ghosh, So
APPLICANT: Davis, RO
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Seattle CITY: Seattle Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                    TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Rosenman Ph.D., S
REGISTRATION NUMBER: 43
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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NO. 6218117
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287 CWLVTEGVCIL---TGLGFNGFEEKGKAKWDACANMKVWLFETNPRFTGTIASFNINTNA 343
                                                                                                                                                                           201 PQFSMNHYMKLVQGELIDIPGKIPNSIIP-----ALKRLSLGLFYLVGYTLLSP 249
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                                                                                                                                                                                                                    54;
                                                         58 DASTAFSSIAHITRDVNYGWIIRYL---HANGASMFFICLFLHIGRGLYYGSFL---YSE 111
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                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----GAFLVGPQFSMNHYMKLVQGELIDIPGKIPNSIIPALKRLSLGLFYLVGYTLLSP 249
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                                                                                                                                    PMRKINPLMKLINHSFIDLP--TPSNISAWWNFGSLLGACLILQITTGLFLAMHY---SP
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Ghosh, Soumitra S.
Davis, Robert E.
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                  linear
                                                                                             -----HITED-----YLLTEDYDNHPFWFRCMYM-----LIWGKFVLYKYVT 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43,058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stephen J.
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                                                                                                                                                                                                                                      Score 92; I
Pred. No. 0.
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0.24;
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Patent No. 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: ROSENMAN Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 660088.416
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1050RMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOPTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA: APPLICATION UMBER: US/09/098,07: FILLING DATE: 15.-UN-1998 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Fahy, Eoin F.
APPLICANT: Davis, Robert E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: C. Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
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344 WVARYIFKRLKFLGNKELSQGLSLLFLALMHGLHSGYLVCFQMEFLIVIVERQAARLIQE 403
                                                                          287 CWLVTEGVCIL---TGLGFNGFEEKGKAKWDACANMKVWLFETNPRFTGTIASFNINTNA 343
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                                                                                                                                                                                     3 PMRKINPLMKLINHSFIDLP--TPSNISAWWNFGSLLGACLILQITTGLFLAMHY---SP 57
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                                                                                                               DASTAFSSIAHITRDVNYGWIIRYL---HANGASMFFICLFLHIGRGLYYGSFL---YSE 111
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                                        TWNI--GIILLLATMATAFMGY----VLPW---GOMSFW----
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                                                                                                                                                                                                                                                                                                                                                                                                                     380 amino acids
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Ghosh, Soumitra S.
Clevenger, William
                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                  DB 4; Length 380;
0.24;
                                                                                                                                                                                                                                                                 75; Indels 108;
                                      ----GA 143
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Search completed: November 21, 2003, 14:17:10 Job time: 22 secs

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RESULT 15
US-09-328-352-5397
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APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5397
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Patent No. 6562958
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Best Local Similarity 21.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 470
TYPE: PRT
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328
                                                                                                                                                                                                                                                                                                                                                                               195 GAFLVGPQFSMNHYMKLVQGELID-IPGKIPNSIIPALKRLSLGLFYLVGYTLLSPHITE 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 DIKWTM--PHCVLTLKLIGLAVDYFDGGKDQNSLSSEQQKYAIRGVPSLL-EVAGFSYFY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66;
                                                                                                                          GLSLLFLALWHGLHSGYLV----CFQMEFLIVIVERQAA------RLIQESPTL----
                                                                                                                                                                                                                                                                                                                                        SG--TGAYFG-DLSKAMLNGVAFDALSGTIPESLFVIFQM----TFAIITVAILSGSIA- 184
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SGAVAGLVVITP
                                         -SKLAAITVLOP 418
                                                                                   GAŚLLWVG-WFGFNGGSALGAGARASMAILVTQVAAAAAAFSWLVVERMIRGKASVLGGA 327
                                                                                                                                                                    AADG----WLFKAGALDFAGGTVVHINSGVAGLVAAYMLGKRIGLGRESMAPHNLTLTVI 268
                                                                                                                                                                                                           DACANMKVWLFETNPR--FTGTIASFNINTNAWVARYIFKRLKFLGNKELSQ------
                                                                                                                                                                                                                                                                                              DYLLTEDYDNHPFWFRCMYMLIWGKFVLYKYVTCWLVTEGVCILTGLGFNGFEEKGKAKW 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative . 46; Mismatches
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                                                                                                                                                                                                                                                       -DRMKYSAFMAFIAIW-VLVVYAPITHWV----
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Result
No.
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Maximum Match 100%
Listing first 45 s
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Maximum DB
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                                                                                                                   Pred. No. is the number of results predicted by chance to h score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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-6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
-6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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US-10-024-298A-77	US-09-919-039-200	-09-9	US-10-176-847-40	US-09-898-533-2	US-09-510-332-135	N	US-09-963-766-6	US-09-912-020-378	US-09-741-669-370	US-09-976-605-6	US-09-801-368-244	US-08-879-337-8	US-09-843-598-11		US-10-090-455-2	0-154-452-	-10-154-452-	-10-072-621-	-10-0	-10-090-455-	US-09-922-225A-12	-10-000	S	US-09-510-332-121	-10-1	US-09-796-720B-4	US-09-881-752A-76	US-09-815-242-10225	US-09-876-997-287
	200,	108,	40,	2,	139	129	<u>ب</u>	Sequence 378, App	370	'n	Sequence 244, App		11, Apr	390	ν,	æ	4.	۰,	2		12,	ν,	25,	Sequence 121, App	24	4	e 76,	10225,	Sequence 287, App

#### ALIGNMENTS

PRIOR APPLICATION NUMBER: 09/311,894
PRIOR FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PERL Program
SEQ ID NO 6
LENGTH: 487
TYPE: PRT
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte Clone 1928920 á 밁 á US-09-938-803-6 US-09-938-803-6 Query Match Best Local Similarity Matches 487; Conserva Sequence 6, Application US Patent No. US20020076762A1 APPLICANT: Azimzai, Yalda TITLE OF INVENTION: FULL-LENGTH EXPRESSED GENETIC MARKERS FILE REFERENCE: PF-0695 US CURRENT APPLICATION NUMBER: US/09/938,803
CURRENT FILING DATE: 2000-08-24 APPLICANT: Yue, Henry APPLICANT: Tang, Y. Tom APPLICANT: INFORMATION: 1 MASSAEGDEGTVVALAGVLQSGFQELSLNKLATSLGASEQALRLIISIFLGYFFALFYRH 60 61 YLFYKETYLIHLFHTFTGLSIAYFNFGNQLYHSLLCIVLQFLILRLMGRTITAVLTTFCF 120 MASSAEGDEGTVVALAGVLQSGFQELSLNKLATSLGASEQALRLIISIFLGYPFALFYRH Reddy, Roopa Baughn, Mariah R. Yang, Junming Application US/09938803 Tang, Y. To Lal, Preeti Conservative 100.0%; Score 2580; DB 9; Length 100.0%; Pred. No. 8.9e-239; tive 0; Mismatches 0; Indels 0 Gaps 60

99.5 96.5 95.5

US-09-815-242-5694 US-09-815-242-12667 US-09-731-872-287

US-09-864-761-33415 12 US-10-205-219-19-19-12 US-09-821-812-7-12 US-10-287-274-375 12 US-10-202-824-6 12 US-10-202-824-6 12 US-99-769-787-119-80-5 12 US-09-781-880-5

Sequence 6, Appli Sequence 29742, A Sequence 9, Appli Sequence 9, Appli Sequence 192, App Sequence 17, Appli Sequence 7, Appli Sequence 6, Appli Sequence 6, Appli Sequence 13958, A Sequence 119, App Sequence 5694, Apli Sequence 12667, A

US-09-938-803-6

US-10-029-386-29742 US-09-821-812-9

409

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Sequence 6, Application US/10053248
PUBLICATION NO. US20030144188A1
GENERAL INFORMATION:
APPLICANT: Lin, Biaoyang
TITLE OF INVENTION: Androgen Regulated Nucl
TITLE OF INVENTION: Molecules and Encoded FILE REFERENCE: P.IS 4814
CURRENT APPLICATION NUMBER: US/10/053,248
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
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Matches 108; Conserv
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                           QYERTEPSPHTAV-VQKLLVCGLSLLFHLTICTT-LPVEYNIDEHFQATASWPTKIIYLY
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                                        IWGKFVLYKYVTCWLVTEGVCILTGLGFNGFEEKGKAKWDACANMKVWLFETNPRFTGTI
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Pred. No. 6.3e-25;
(2; Mismatches 177;
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                       Nucleic Acid
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SIN
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: ABOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine ve
SEQ ID NO 29742
LENGTH: 57
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US-10-029-386-29742
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                                                                                                                                                                     Sequence 9, Application US/09821812
Publication No. US20030166520A1
GENERAL INFORMATION:
APPLICANT: Lin, Biaoyang
TITLE OF INVENTION: Androgen Regulated
TITLE OF INVENTION: Nucleic Acids
FILE REFERENCE: P-IS 4373
                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29742, Application US/10029386 Publication No. US20030194704A1
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Best Local
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                                                                                                              CURRENT APPLICATION NUMBER: US/09/821, CURRENT FILING DATE: 2001-03-28 NUMBER OF SEQ ID NOS: 11
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TYPE: PRT
                       ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                      292 EGVCILTGLGFNGFEEKGKAKWDACANMKVWLFETNPRFTGTIASFNINTNAWVAR 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410 LTFYSSWYYCLHILGILVLLLLP 432
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                                                                                                                                                                                                                                                                                                                                                                                   EGVCILTGLGFNGFEEKGKAKWDACANMKVWLFETNPRFTGTIASFNINTNAWVAR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKVYKSIYFLGHIFFLSLLFILP
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NN: EXPRESSED IN PLACENTA, SIGNAL = 3.7

NN: EXPRESSED IN HARIN, SIGNAL = 3.7

NN: EXPRESSED IN HEARIN, SIGNAL = 4.4

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 6.8

NN: EXPRESSED IN BONE MARROW, SIGNAL = 3.1

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 4.6

NN: EXPRESSED IN HELA, SIGNAL = 4.5

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; Pred. No. 2.5e-22;
0; Mismatches 0;
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US-09-864-761-33415
; Sequence 33415, Application US/09864761
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
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CURRENT FILING DATE: 2001-05-23
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LOCATION: (1)...(425)
OTHER INFORMATION: Xaa = Any Amino Acid
                                         APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/207,456
  APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
                                                                                        APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                                                                               FILING DATE: 2001-01-30
                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                        FILING DATE: 2001-01-30
                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 EQQKYAIRGVPSLLEVAGFSYFYGAFLVGPQFSMNHYMKLVQGELIDIPGKIPNS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 YERTXAISKCKVMRFIWSLYSMYXTAXVQKLLVCGLSLLFHLTICTT-LPVEYNIDEHFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322 WLFETNPRFTGTIASFNINTNAWVARYIFKRLKF 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 ATASWPTKIIYLYISLLAARPKYYFAWTLADAINNAAGFGFRGYDENGAARWDLISNLRI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 NHPFW-FRCMYMLIWGKFVLYKYVTCWLVTEGVCILTGLGFNGFEEKGKAKWDACANMKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 -----IIPAL-----KRLSLGLFYLVGYTLLSPHITEDYLLTEDYD 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70
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25.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 231; DB 12;
Pred. No. 1.3e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Annomax Sequence Listing Engine vers. SEQ ID NO 33415
LENGTH: 58
                                                                                                   Query Match
                                                                                                                                                                                                                                                SOFTWARE: Pa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: GB 0118354.0 PRIOR FILING DATE: 2001-07-27 NUMBER OF SEQ ID NOS: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21 PRIOR APPLICATION NUMBER: US 09/608,408 PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/205,219
CURRENT FILING DATE: 2002-07-24
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pinnock, Robert TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain FILE REFERENCE: WL-A-018200
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Warner-Lambert Company APPLICANT: Lee, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                   TYPE: PRT
ORGANISM: Rattus norvegicus
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OTHER
                                                                                                                                                           OTHER INFORMATION: BB1
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                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391 VIVERQAARLIQESPTLSKLAAITVLQPFYYLVQQTIHWLFMGYSMT 437
                                 226 SIIPALKRL----SIGLFYLVGYTLLSPHITEDYLLTED-YDNHPFWFRCMYML-IWGKF 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 LLLPPQAARLIQESPTLSKLAAITVLQPFYYLVQQTIHWLFMGYSMT 58
                                                                                                                                                                                                                               342
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42; Conserv
                                                                                   Similarity
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SLRPLLRRAWPAPLFGLLF-----LLSSHLFPLEAVREDAFYARPLPARLFYMIPVFFAF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                              Dixon, Alistair
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D IN FETAL LIVER, SIGNAL = 11
D IN HELA, SIGNAL = 3.5
D IN ADULT LIVER, SIGNAL = 6.9
D IN BT474, SIGNAL = 5.9
D IN HEART, SIGNAL = 5.9
D IN HEART, SIGNAL = 2.0
D IN HEART, SIGNAL = 2.00-26
N HIT: W25367.1, EVALUE 3.000-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIT: W26367.1, EVALUE 3.00e-26
HIT: P43288, EVALUE 4.50e+00
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IN BONE MARROW, SIGNAL = 3.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IN LUNG, SIGNAL = 5.5
IN BRAIN, SIGNAL = 2.
IN PLACENTA, SIGNAL =
                                                                  Score 150; DB 12;
Pred. No. 5.9e-06;
5; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 215; DB 9;
Pred. No. 3.3e-13;
3; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL = 2.2
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                                                                                                   Length 342;
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VLYKYVTCWLVTEGVCILTGLGFNGFEEKGKA------KWDACA 317

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Length 392;

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; TYPE: PRT ; ORGANISM: Escherichia coli US-10-287-274-375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-812-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-287-274-375
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US-09-821-812-7
                                                                                                      PRIOR APPLICATION NUMBER: US 60/164415
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: US 09/711164
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/821,812
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09821812
Publication No. US20030165520A1
GENERAL INFORMATION:
APPLICANT: Lin, Biaoyang
TITLE OF INVENTION: Androgen Regulated Prostate Specific
TITLE OF INVENTION: Nucleic Acids
FILE REFERENCE: P-IS 4373
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 375, Application US/10287274 Publication No. US20030181408A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
                                                                                                                                                                                                                                                       APPLICANT: Forsyth, R. Allyn
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETC
FILE REFERENCE: ELITRA.008DV1
CURRENT APPLICATION NUMBER: US/10/287,274
CURRENT FILING DATE: 2002-10-31
                                                                                    LENGTH: 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 FCFQMAYL----LAGYYYTATGNYDIKWTMPHCVLTLKLIGLAVDYFDG--GKDQNSLSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.8%; Score 123.5; DB 1
31.1%; Pred. No. 0.00063;
ative 19; Mismatches 45
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US-10-202-824-6
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Best Local Similarity
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                    INFORMATION
                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTMARE: PECENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/202,824
PILING DATE: 26-Jul-2002
CLASSIFICATION: Unknown>
                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/669,656
FILING DATE: 24-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
                                                           REFERENCE/DOCKET NUMBER: PHM.70086 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Akopian, Armen N. TITLE OF INVENTION: Ion Chan NUMBER OF SEQUENCES: 31
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 DIKWTMPHCVLTLKLIGLAVDYFDGGKDQNSLSSEQQ-----KYAIRGVPSLLEVAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1800 Concord Pike, P.O. Box 15437 CITY: Wilmington STATE: Delaware
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                  TELEPHONE: (302) 886-7466
N FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
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Pred. No. 0.039;
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TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-202-824-6
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US-09-815-242-13958
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Best Local Similarity
Matches 113; Conserv
                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                        APPLICANT:
TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                             APPLICANT: Haselbeck, Robert
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                                                                                                                                                                         Ohlsen, Kari L.
Zyskind, Judith W.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VWNGEKLRWHMCDFFHSFLVV
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                                                                                                                                                           Xu, H. Howard
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                                                                                                                                         Genes
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  RESULT 11
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; LOCATION: (1)...(613)
; OTHER INFORMATION: Xaa =
US-09-815-242-13958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version SEQ ID NO 13958
LENGTH: 613
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Best Local Similarity
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/207,727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 ALFILYNELGTLNFREMVELAPAHFADGNNMLMWA-----TLMLLGGAV-----GKSAQ 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 GPVLLAFSRGRWSENLSATIGVGSVGLAALVTAFVGMDF--FANGKQAFSQPLWTWMSVG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 GPQELSLNK-----LATSLGASEQALRLIISIFLGYPFALFYRHYLFYKET-----
                                                                                                                                                                                                                                                                                                                                                                      MTHAF-FKALLFLASGSVILACHHEQNIFKMGGLRKSIPLVYACFLVGGAALSALPLVTA 394
                                                                                                                                                                                                                                                                                                                                                                                                          -NHPFWFRCMYMLIWGKFVL-----YK-----YVTCWLVTEGVCILTGLGFN 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLSSEQQKYAIRG---VPSLLEVAGFSYFYGAFLVGPQFSMNHYMKLVQGELIDIPGKIP 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VL-QFLILRLMGRTITAVLTTFCFQMAYLLAGYYYT-------
                                                          --WYNAW-----GEDWLYDKVFVKPFLGIAWLLKRDPLNAL
                                                                                               DKWLKVYKSIYFLGHIFFLSLLFILPYIHKAMVPRKEKLKKM 486
                                                                                                                                                                                                                                                    GLSLLFLALWHG-----LHSGYLVCFQMEFLIVIVERQAARLIQESPTLSKLAAITVLQP 418
                                                                                                                                                                                                                                                                                                                             GFEEKGKAKWDACANMKVWLFETNPRFTGTIASFNINTNAWVARYIFKRLKFLGNKELSO 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPLQTWLADAMAGPTPVSALIHAATM-VTAGVYLI----ARTHGLFLMTPEILHLVG---
                                                                                                                                                                           FYYLVQQTIH----
                                                                                                                                                                                                                                                                                           GFFSKDEILAGAMANGHI-----NLMVAGLVGAF--MTSLYTFRMIF-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLSDNLLLMYLGWEGVGL------CSYLLIGFYYSDPKNGAAAMKAFVVTRVGDVFLAF 183
                                                                                                                                     LQGVLPQTTELAHGRVLTLEITSGVVAIAGIXIAAWLWLGXRTLVTSIAXSAPGHLLGTW
                                                                                                                                                                                                                -----IVFHGKEXIHAHAGKXITHHLPLIVLMI------
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17.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-769-787-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-781-880-5
                                                                                      US-09-781-880-5
                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09781880
Publication No. US20030166042A1
GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
                                                                                                                                             PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5
LENGTH: 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
SEQ ID NO 119
LENGTH: 263
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Best Local Similarity
  Matches 108;
                   Query Match
Best Local
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                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/781,880
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/182,061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: No. US20030166042A1el Seven-Transmembrane TITLE OF INVENTION: Proteins/G-Protein Coupled Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: GB 9816337.1 PRIOR FILING DATE: 1998-03-27
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                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 AFLVGPQFSMNHYMKLVQGELIDIPGKIPNSIIPALKRLSLGL-----FYLVGYT-- 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 SIPCLIYLVTVLIIAIITYFFGTFSPLGWNSLFSDGS-----GLQRLLDGEIKSYLFFTC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 MQASYGDVSLMKLFTPYİLYIVPYMVLEKYEDN 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 FFALFYRHYLFYKETYLIHLFHTFTGLSIAYFNF------GNQLYHSLLCIVLQF
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                      Similarity
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o. US20030091577A1
3.9%; Scilarity 21.1%; Pr
Conservative 62;
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Score 99.5; DB 12;
Pred. No. 0.99;
2; Mismatches 196;
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  Indels 147;
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RESULT 13
US-09-815-242-5694
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                                        Sequence 5694, Application US/09815242 Patent No. US20020061569A1
                      INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 HTFTGLSIAYF-----NFGNQLYHSLLCIV----LQFLILRLMGRTITAVLTTFCF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 QBLSLNKLATSLGASEQALRLI-----ISIFLGYPFALFYRHYLFYKETYLI--HLF
                                                                                                                                                                                                                 SIYFLGHIFFLSLLFILPYIHKAMVPRKEKLKK 485
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Haselbeck, Robert
                                                                                                                                                                                                                                                                                                     RQAARLIQESPTLSKLAAITVLQPFYYLVQQTI---HWLFMGYSMTAFCLFTWDKWLKVYK 452
                                                                                                                                                                                                                                                                                                                                                                                        ASFNINTNAWVARYIFKRLKFLGNKELSQGLSLLFLALWHGLHSGYLVCFQMEFLIVIVE 394
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PELICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16 GENERAL INFOI APPLICANT: I NUMBER OF SEQ ID N SOFTWARE: FastSEQ SEQ ID NO 5694 TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA,011A PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26 CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Carr, Grant J. Yamamoto, Robert T. Xu, H. Howard Ohlsen, Kari L. Zyskind, Judith Wall, Daniel Trawick, John D. ID NOS: 14110 SEQ for Windows Σ Version

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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION UNMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR APPLICATION NUMBER: 60/207,727
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; ORGANISM: Staphylococcus aureus
US-09-815-242-5694
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Best Local Similarity
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SEQ ID
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                                       NUMBER OF SEQ ID NOS: 14110
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                    SOFTWARE: FastSEQ for Windows Version 4.0
NO 12667
                                                         APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
                                                                                                                          APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                             FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
                                                                                                          FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 ----QFAIEPLKHLWSLAIEEQFYLLFPLVITFLLHRFK-------PRNIIQT 170
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Yamamoto, Robert T
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Trawick, John D.
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Zyskind, Judith W.
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21.0%; Pred. No. 1.
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                                                                                                                                                                       US-09-731-872-287
                                                                                                                                                                                                                                                                              · SOFTWARE: Patent.pm
SEQ ID NO 287
LENGTH: 286
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US3.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 287, Application US/09731872 Patent No. US20020102604A1
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CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/187,470 PRIOR FILING DATE: 2000-03-06
                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 482
                                                                                                                                                                                     PEATURE:
NAME/KEY: SIGNAL
LOCATION: -48..-1
                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                          161 DGGKDQNSLSSEQQKYAIRGVPSLLEVAGFSYFYGAFLVGPQFSMN---HYMKLVQGELI 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 DISKKIVVS----LDIIĞISĞFAVL-MTLFFIVGDQDQWIY--NGGFYIISFATLFIIAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 L---KRLSLGLFYLVGYTLLSPHITED----YLLTEDYDNHPFWFRCMYMLIWGKFVLYK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 LIFKPELIIQMKRDAIAAIFYVSNWWY------ISQNVDYFN------
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                                                                                     l Similarity
76; Conserv
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                                                                                  3.7%; Score 95.5; DB 10; 22.1%; Pred. No. 0.78; tive 39; Mismatches 102;
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Pred. No. 1.7;
2; Mismatches 138; Indels 103;
                                                                                                                           Length 286;
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    62
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Search completed: November 21, 2003, 14:21:38 Job time: 37 secs

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Minimum DB
Maximum DB
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Gapop 60.0 , Gapext 60.0
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487
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

9	8	7	6	U	4.	ω	2	ų	Regult No.
42	42	42	42	123	303	487	487	487	Score
8.6	8.6	8.6	8.6	25.3	62.2	100.0	100.0	100.0	Query Match Length
58	58	58	58	128	424	487	487	487	
22	22	22	22	21	22	22	22	21	B
ABB18117	ABB32619	ABB27468	ABG47472	AAG00235	ABG06198	AAB36584	AAB31669	AAY69987	DB ID
Protein #116 encod	Peptide #125 encod	Human peptide #119	Human liver peptid	Human secreted pro	Novel human diagno	Human FLEXHT-6 pro	Amino acid sequenc	Human receptor-ass	Description

				r		
ATP-binding casset	AAU04308	22	21	1.4	7	45
	AAE30406	24	20	1.4	7	44
Hll binding site c	AAM44243	22	7	1.4	7	43
	AAM44238	22	7	1.4	7	42
Human P-gp mutant,	AAE18979	23	1280	1.6	œ	41
	AAE18969	23	1280	1.6	æ	40
ס	ABB66357	22	1252	1.6	œ	39
	AAB25105	21	947	1.6	<b>&amp;</b>	38
albic	ABP73457	23	609	1.6	æ	37
Soybean CDPK prote	AAW93256	20	512	1.6	œ	36
Human G protein-co	AAU19246	22	317	1.6	œ	35
<ul> <li>Arabidopsis thalia</li> </ul>	AAG22431	21	310	1.6	œ	34
	AAG22432	21	278	1.6	80	33
0	AAG22433	21	246	1.6	œ	32
ř	AAP60957	7	111	1.6	œ	31
P patens lipid met	AAG83328	22	90	1.6	œ	30
0	AAG80879	22	90	1.6	œ	29
~	ABJ05411	23	86	1.6	œ	28
20	ABJ05408	23	86	1.6	œ	27
٥	ABJ05404	23	86	1.6	œ	26
Σ	ABJ05397	23	86	1.6	8	25
Duck acyl coenzyme	ABJ05395	23	86	1.6	œ	24
Chicken acyl coenz	ABJ05390	23	86	1.6	8	23
Recombinant bovine	AAR11874	12	86	1.6	œ	22
	AAP60954	7	86		æ	21
	ABB60158	22	556		9	20
Amino acid sequenc	AAY13453	20	556	1.8	9	19
Propionibacterium	AAU45415	22	276	1.8	ø	18
_	AAM06401	22	47	1.8	9	17
	ABG06197	22	267	2.7	13	16
eptide	ABG35460	23	58	•	42	15
#120	AAM01438	22	58	8.6	42	14
#125	AAM26088	22	58	٠	42	13
	AAM13688	22	58		42	12
	AAM65826	22	58	8.6	42	11
Human brain expres	AAM53449	22	58	8.6	42	10

# ALIGNMENTS

K F X	F F F	FT	FH	% %	ŽΧ̈́	ΚW	\(\frac{1}{2}\)	Ş	Κ¥	<b>2</b> 2	¥	ž	Z X	DT	X	AC A	<b>4</b> E	AAY6	RESULT
"Potential phosphorylation	/note= "Potential phosphorylation site"  Modified-site 149  /note= "Potential phosphorylation site"		Key Location/Qualifiers Modified-site 3	Homo sapiens.		arthritis; anaemia; asthma; dermatitis; diabetes; osteoporos	<pre>cardiovascular; cell proliferative; autoimmune; inflammatory gastrointestinal; atherosclerosis; cirrhosis; leukaemia; can</pre>		antiasthmatic; osteopathic; antiallergic; antidiabetic; derm	<pre>cytostatic; immunomodulatory; antiinflammatory; cardiant; an antiarteriosclerotic; hepatotropic; antiarthritic antirheuma</pre>	Human receptor-associated protein; HRAP; Incyte clone 290697	The state of the s	Himan recentor-accomiated protein from Incyte clone 2006071	31-MAY-2000 (first entry)		AAY69987;	AAI6996/ BCANGAIG; PIOCEIN; 48/ AA.	87	IJT 1

Human receptor-associated protein; HRAP; Incyte clone 2906971; cytostatic; immunomodulatory; antiinflammatory; cardiant; antianaemic; antiarteriosclerotic; hepatotropic; antiarthritic antirheumatic; antiasthmatic; osteopathic; antiallergic; antidiabetic; dermatological; neuroprotective; diagnosis; treatment; prevention; reproductive disorder; cardiovascular; cell proliferative; autoimmune; inflammatory; allergy; gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS; arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis; multiple sclerosis; irritable bowel syndrome.

# Homo sapiens.

_	/no Modified-site 235	/noi Modified-site 149	/no Modified-site 183	Key Loc Modified-site 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell proliferative, autoimmune/inflammatory, reproductive, cardiovascular and gastrointestinal disorders (e.g. atherosclerosis, circles, elukaemia, cancer, AIDS, arthritis, allergies, anaemia, circles, anaemia, cancer, AIDS, arthritis, allergies, anaemia, circles, anaemia, cancer, AIDS, arthritis, allergies, anaemia, circles, circles, circles, circles, circles, circles, circles, circles, circles, circles, circles, circles,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiinflammatory, cardiant, antiarteriosclerotic, hepatotropic, antialrathritic, antirheumatic, osteopathic, antialregic, antianaemic, antialathoric osteopathic, antialregic, antianaemic, antidiabetic, dermatological and neuroprotective activities. The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with HRAP expression, especially call proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Pages 73-74; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human receptor-associated proteins (HRAP) useful for the diagnosis, treatment and prevention of cell proliferative, autoimmune, inflammatory, reproductive, cardiovascular, and gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAZ50889
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01-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is expressed in nervous, gastrointestinal and reproductive tissues. HRAP has cytostatic, immunomo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present (HRAP) from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-205710/18
361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MASSAEGDEGTVVALAGVLQSGFQELSLNKLATSLGASEQALRLIISIFLGYPFALFYRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seent sequence is a human receptor-associated protein from Incyte clone 2906971 obtained from THYMNOTO5 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLFYKETYLIHLFHTFTGLSIAYFNFGNQLYHSLLCIVLQFLILRLMGRTITAVLTTFCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLFYKETYLIHLFHTFTGLSIAYFNFGNQLYHSLLCIVLQFLILRLMGRTITAVLTTFCF
                                LSQGLSLLFLALMHGLHSGYLVCFQMEFLIVIVERQAARLIQESPTLSKLAAITVLQPFY
                                                                                                                                     GFNGFEEKGKAKWDACANMKVWLFETNPRFTGTIASFNINTNAWVARYIFKRLKFLGNKE
                                                                                                                                                                                                            LVGYTLLSPHITEDYLLTEDYDNHPFWFRCMYMLIWGKFVLYKYVTCWLVTEGVCILTGL
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                                                                                                       GFNGFEEKGKAKWDACANMKVWLFETNPRFTGTIASFNINTNAWVARYIFKRLKFLGNKE
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                                            The protein possesses a hydrophobic domain and so is a secretory protein or a membrane protein. The protein is used as an antigen to prepare antibodies. The polynucleotide sequence is useful as a source of probes for genetic diagnosis. It is also useful as a source of probes for genetic diagnosis. It is also useful for producing the protein in large quantities and for gene therapy. The eukaryotic cells are used for detecting the receptors or ligands corresponding to the protein and for detecting small novel pharmaceuticals. The antibodies are also used for detection, quantification and purification of the proteins. Both the protein and polynucleotide may be used in research or as nutritional sources or supplements. The protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, hematopoiesis regulating activity, tissue growth activity, activity, and tumour inhibition activity, receptor/ligand activity, anti-inflammatory activity and tumour inhibition activity, anti-inflammatory treatments of immune deficiencies resulting from autoimmune disorders or infectious diseases, Parkinson's disease, induce fertility, improve
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated human proteins and polynucleotides are used in research and have activities including cell proliferation/differentiation activity immune stimulating activity and receptor/ligand activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; hydrophobic tumour inhibition;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 90-93; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kato
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parkinson's disease; fertility; immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a human protein with hydrophobic domains
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tumour inhibition; immune deficiency; autoimmune disorder; anaemia;
infectious disease; cancer; ulcer; periodontal disease; coagulation;
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                                    mmune response and
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                                    enhance coagulation or inhibit thrombosis
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er; anaemia; burn;
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Query Match Best Local Similarity

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                       14 HMAY-1999;
14 HMAY-1999;
14 HMAY-1999;
                                                                                                                                                                                                                                                                                                        Human; FLEXHT; full-length molecules expressed in human tissue; diagnosis; gene expression; genetic linkage; genetic variability; antianaemic; anticonvulsant; antiarteriosclerotic; immunomodulatory; cytostatic; antito; antiinflammatory; hepatotropic; antidiabetic; anti-gout; antithyroid; neuroprotective; antiarthritic; osteopathic; antipsociatic; antixheumatic; antiulcer; gene therapy; anaemia; gout; epileps; arteriosclerosis; atherosclerosis; developmental disorder; cancer; immunological disorder; asthma; bronchitis; cirrhosis; crohn's disease; diabetes mellitus; Grave's disease; multiple sclerosis; osteoarthritis; pancreatitis; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                                                                                                            ulcerative colitie.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human FLEXHT-6
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                                                                                                             12 HMAY - 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                LSQGLSLLFLALWHGLHSGYLVCFQMEFLIVIVERQAARLIQESPTLSKLAAITVLQPFY
                                                                                                                                                                                                                           GFNGFEEKGKAKWDACANMKVWLFETNPRFTGTIASFNINTNAWVARYIFKRLKFLGNKE
                                                                                                                                                                                                                                                                                                                 LVGYTLLSPHITEDYLLTEDYDNHPFWFRCMYMLIWGKFVLYKYVTCWLVTEGVCILTGL
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                  YLVQQTIHWLFMGYSMTAFCLFTWDKWLKVYKSIYFLGHIFFLSLLFILFYIHKAMVFRK
                                                            YLVQQTIHWLFMGYSMTAFCLFTWDKWLKVYKSIYFLGHIFFLSLLFILPYIHKAMVPRK
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                                                                                                                                                                                                 GFNGFEEKGKAKWDACANMKVWLFETNPRFTGTIASFNINTNAWVARYIFKRLKFLGNKE
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                                                                                                                 polymerase chain reaction (PCR) primers, and for chromosome and gene mapping, and in recombinant production of [II]. The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. [I] is useful in gene therapy techniques to restore normal activity of [II] or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. [II] and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences of the invention.
                                                Query Match
Best Local S
Matches 303
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                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences (I) is useful as hybridisation probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20;
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                                                                                                                                                              specification,
                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
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64 YKETYLIHLEHTETGLSIAYENFGNOLYHSLLCIVLOFLILRLMGRTITAVLTTFCFOMA
                                                               Similarity
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                                                                                                                                                             sequence data for this patent did not tion, but was obtained in electronic for
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                                                                        The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed CDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
                                                                                                                                                                                                                                                                   New nucleic acid that is a 5' expressed sequence tag (5' EST) obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and diagnostic, forensic, gene therapy and chromosome mapping prodi
                        ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream
                                                                                                                                                                                                                                       Claim 13; SEQ ID 4316; 71pp + CD-ROM; English
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N-PSDB; AAC00241.
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from WIP
                                                                                                   The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleocide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348.ABG59930 represent
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26-MAY-2000;
30-JUN-2000;
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                          human liver single exon encoded peptides of the invention.
Note: The sequence information for this patent does not appear in the
printed specification but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful analysing gene expression in human adult liver -
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                                                                    CC The invention relates to a spatially-addressable set of single exon CC nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting CC from human breast and BT 474 cells. The method involves contacting CC derived from mRNA of human breast, and then measuring the label CC derived from mRNA of human breast, and then measuring the label CC condit to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to CC encode proteins. They are useful for gene discovery, and for CC expression analysis is useful for prognosing breast disease. Gene CC expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater CC diversity of probes for measuring gene expression, with far less bias CC than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The Drobe of the invention present sequence is a peptide encoded by a single exon nucleic acid
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Best Local Similarity
Matches 42; Conser
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03-AUG-2000;
21-SEP-2000;
          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format dirfrom WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                            New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; microarray; single exon probe; gene expression; breast;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB27468 standard; Peptide; 58
                                                             probe of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human peptide #119 encoded by breast cell single exon nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396 QAARLIQESPTLSKLAAITVLQPFYYLVQQTIHWLFMGYSMT 437
                                                                                                                                                                                                                                                                                                                                             27; SEQ ID NO 10436;
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2000US-0632366.
2000US-0234687.
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2000GB-0024263.
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Pred. No.
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RESULT 8
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RESULT 9
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Matches
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26-MAY-2000; 2000US-0209496.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234587.
27-SEP-2000; 2000US-023659.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                       The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from wIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome-derived single exon nucleic zing gene expression in human fetal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        foetal liver; gene expression; single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULAR DYNAMICS INC.
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2000US-0608408,
2000US-0632366,
2000US-0234687,
2000US-0234687,
2000US-0236359,
2000GB-0024263.
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58
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Pred. No. 2.7e-32;
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Pred. No.
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                                                                                                                                                                                                                            Length 58;
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RESULT 10
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ID AAM53
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DT 05-NO
XX
DE Human
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                             measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one sucl probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB18117 standard; Protein; 58
                                         05-NOV-2001
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                                                                                               AAM53449 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-)
                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
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                                         (first entry)
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                                                                                             Protein;
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2.7e-32;
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                          The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
04 FEB-2000;
26-MAY-2000;
                             30-JAN-2001; 2001WO-US00668
                                                                      WO200157276-A2
                                                                                          Homo
                                                                                                            microarray; cancer;
                                                                                                                        Human; bone
                                                                                                                                           Human bone
                                                                                                                                                                06-NOV-2001
                                                                                                                                                                                    AAM65826;
                                                                                                                                                                                                       AAM65826 standard;
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-)
                                                                                                                                                                                                                                                                                                                                                             probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-483446/52.
                                                                                                                                                                                                                                                                              396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SG,
                                                                                         sapiens
                                                                                                                                                                                                                                                          17
                                                                                                                                                                                                                                                                                                  42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                       QAARLIQESPTLSKLAAITVLQPFYYLVQQTIHWLFMGYSMT 437
                                                                                                                                                                                                                                                        QAARLIQESPTLSKLAAITVLQPFYYLVQQTIHWLFMGYSMT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanzel
                                                                                                                                           marrow
                                                                                                                                                                                                                                                                                                                                           58
                                                                                                                                                                                                                                                                                                                                                             of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0234685.
; 2000US-02346359.
                                                                                                                        marrow
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          invention
2000US-0180312
2000US-0207456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001WO-US00667
                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                           8
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                                                                                                                                          expressed
                                                                                                                     expressed exon; gene expression
                                                                                                                                                                                                       Protein;
                                                                                                                                                               entry)
                                                                                                              leukaemia;
                                                                                                                                                                                                                                                                                                           8.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                          provides
                                                                                                                                                                                                                                                                                                                                                                                                                                           25554; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen W,
                                                                                                                                           probe
                                                                                                                                                                                                       58
                                                                                                                                                                                                                                                                                                 <u>.</u>
                                                                                                                                                                                                                                                                                                           Score 42;
Pred. No.
                                                                                                                                                                                                       ₽
                                                                                                                                                                                                                                                                                                                                                                                                                         a number of single exon
                                                                                                              lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank DR;
                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for analyzing
                                                                                                                                         encoded protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                           DB 22; |
2.7e-32;
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                                                                                                                                                                                                                                                                                                                   Length 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic
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                                                                                                                                           26132.
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RESULT 12
AAM13688
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Best Local
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       samples,
       Human genome-derived analyzing gene expres
                                                                                                               21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                           09-AUG-2001.
                                                                                                                                                                                                                                                                        cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4;
                                                                                                                                                                                      30-JAN-2001;
                                                                                                                                                                                                                                WO200157278-A2
                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                 Probe; human;
                                                                                                                                                                                                                                                                                                      Peptide #122 encoded by probe for measuring cervical
                                                                                                                                                                                                                                                                                                                           12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                     AAM13688 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probes which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analyzing
                                                                                (MOLE-)
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                                                            SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                           396 QAARLIQESPTLSKLAAITVLQPFYYLVQQTIHWLFMGYSMT 437
                                                                                                                                                                                                                                                                                                                                                                                                                       17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity
42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lymphoma, encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sent invention provides a number of single exon nucleic acid which are derived from genomic sequences expressed in the human frow. They can be used to measure gene expression in bone marrow which may enable the improved diagnosis and treatment of cancers lymphoma, leukaemia and myeloma. The present sequence is a encoded by one of the probes of the invention.
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                                                                                MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                        cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene expression
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                                                            Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58
                                                                                                                                2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
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2000US-0234687.
2000US-0236359.
2000US-0024263.
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                                                                                                              2000US-0234687
2000US-0236359
                                                                                                                                                                                      2001WO-US00670
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                     2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA:
                                                                                                                                                                                                                                                                                 microarray;
       erived single exon nucleic acid probes useful expression in human cervical epithelial cells
                                                           DK,
                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.6%; Su
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26132; 658pp + Sequence Listing;
                                                            Chen W,
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                                                                                                                                                                                                                                                                                 gene
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                                                                                                                                                                                                                                                                                                                                                                     58.
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank
                                                            Rank
                                                                                                                                                                                                                                                                                 expression; cervical
                                                                                                                                                                                                                                                                                                                                                                     ₽
                                                            몄
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; 1
2.7e-32;
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                                                                                                                                                                                                                                                                                 epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                       58
                                                                                                                                                                                                                                                                                                      gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                 for
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Claim 27; SEQ ID No 18514; 487pp; English.

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RESULT 13
AAM26088
 \begin{array}{c} \mathsf{X} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} 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\times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf{C} \times \mathsf
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Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                             The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genetic
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27;
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27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM26088
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                                                                                           human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SG,
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                                                                                           genetic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID No 26357; 654pp; English
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58
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2000US-0632366.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for measuring placental gene expression
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396 QAARLIQESPTLSKLAAITVLQPFYYLVQQTIHWLFMGYSMT 437

QAARLIQESPTLSKLAAITVLQPFYYLVQQTIHWLFMGYSMT

Matches

42;

Conservative

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Query Match Best Local Similarity

8.6%;

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Best Local S
Matches 42
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30-JUN-2000;
03-AUG-2000;
                                                                         The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
  Sequence
                      Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM01438 standard;
                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                       WPI; 2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe; human; breast disease; breast cancer; develo; inflammatory disease; proliferative breast disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM01438;
                                                              breast disease and non-carcinoma tumours
                                                                                                                                                                                                                                            Novel single exon nucleic acid probe used
                                                                                                                                                                                                                                                                                                                                                                          21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                         (MOLE-)
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                                                                                                                                                                                                                                                                                                                          MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                        SEQ ID No 10178; 322pp;
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2000US-0608408.
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Conservative (
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2.7e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human breast gene expression.
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                                      part of the printed directly from WIPO
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RESULT 15
ABG35460
The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived of from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their occupiements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a condicate acid from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung manufactured from human lung from human lung manufactured from human lung manufactured from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lung from human lu
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27; SEQ ID No 25125; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spatially-addressable set of single exon nucleic acid probes, used to meagure gene expression in human lung samples -
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04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human peptide
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2000US-207456P.
2000US-0608408.
2000US-0632366.
2000US-234687P.
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2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58
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12011 sequences,

mentioned in the specification, or encoded by the

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                                                                                                                                                                                           CC probes/open reading frames (ORF). The probes are used for gene capression analysis, and for identifying exons in a gene, particularly CC using human lung derived mRNA and for the study of lung diseases CC such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary (COPD), interstitial lung disease, tuberous sclerosis, Gaucher's disease, (COPD), interstitial lung disease, hermansky-pullak syndrome, sarcoidosis, pulmonary (COPD), pulmonary histiocytosis, lymphangioleiomyomtosis, COPD, lumonary diveolar proteinosis, karagener syndrome, fibrocystic (COPD), printed specification, but was obtained in electronic (COPD), printed specification, but was obtained in electronic (COPD), printed specification, at the corrector (COPD), printed specification, but was obtained in electronic (COPD).
                                                                                             Matches
                                                                                                                                           Query Match
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                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                           Local Similarity
nes 42; Conserv
                                             396 QAARLIQESPTLSKLAAITVLQPFYYLVQQTIHWLFMGYSMT 437
17
QAARLIQESPTLSKLAAITVLQPFYYLVQQTIHWLFMGYSMT
                                                                                                                                                                                           58 AA;
                                                                                             Conservative
                                                                                                                    8.6%;
                                                                                      0,
                                                                                                                    Score 42;
Pred. No.
                                                                                             Mismatches
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. 2.7e-32;
                                                                                                                                        Length 58;
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Search completed: November 21, Job time: 47 secs 2003, 14:22:36

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1 9 1.8 556 2 A32466 prumb protein - fru probable retroelem probable retroelem probable retroelem probable retroelem probable retroelem probable retroelem probable retroelem probable retroelem probable retroelem probable retroelem probable retroelem probable retroelem probable redozepine - bill protein protei	Word size: 0  Total number of hits satisfying chosen parameters: 283308  Minimum DB seq length: 0  Maximum DB seq length: 200000000  Post-processing: Listing first 45 summaries  Database: PIR_76:* 2: pir2:* 3: pir2:* 3: pir3:* 4: pir4:*  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.  SUMMARIES  Result Query  No. Score Match Length DB ID  Description	rotein - prot on: N e: U ect Score: 4 ence: 1 ing table: G ched: 2
Qy 360 ELSQGLSLL 368	RESULT 1 A32466 A32466 C;Species: Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 24-Sep-1998 C;Accession: A32466 R;Uemura, T.; Shepherd, S.; Ackerman, L.; Jan, L.Y.; Jan, Y.N. Cell 58; 349-360, 1989 A;Title: numb, a gene required in determination of cell fate during sensory organ formation organization of cell fate during sensory organ formation organization organization organization of cell fate during sensory organ formation organization organization organization of cell fate during sensory organ formation organization organization of cell fate during sensory organ formation of cell fate durin	30 7 1.4 228 2 F71831 hypothetical prote phosphate uptake r 255 2 AB2740 outer membrane pro 27K outer membrane pro 27K outer membrane pro 27K outer membrane pro 27K outer membrane pro 27K outer membrane 27C 272523 outer membrane 27C 272523 outer membrane 27C 272523 outer membrane 27C 272523 outer membrane 27C 272523 outer membrane 27C 272523 outer membrane 27C 272523 outer membrane 27C 272523 outer membrane 27C 272523 outer membrane 27C 272523 outer membrane 27C 272523 outer membrane 27C 272523 outer membrane 27C 272523 outer membrane 27C 272523 outer membrane 27C 272523 outer membrane 27C 27C 272523 outer membrane 27C 27C 27C 27C 27C 27C 27C 27C 27C 27C

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nypornetical proce	conserved hypothet	glycerol-3-phospha	NH3-dependent NAD	NAD synthetase, pr	NAD synthetase [im		hypothetical prote	hypothetical prote	hypothetical prote	coat protein - tom	27K outer membrane	phosphate transpor	outer membrane pro	phosphate uptake r	hypothetical prote

### ALIGNMENTS

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A;Gene: F25P12.89
                                                                                                                                                                                                                                                                                                                                                                     ; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
hung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,
1908, B.; Huizar, L.
1920, 2000
                                                                                                                                                                                  cer, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, rey, T.; Rowley, D.; Sakano, H.; berg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; Cre and analysis of chromosome 1 of the pais, R.W.; berg, A86141; MUID:21016719; PMID:11130712
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                                               minary
:: DNA
486 <STO>
:ces: GB:AE005173; NID:g9954746; PIDN:AAG09097.1; GSPDB:GN00141
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Conservative 0; Mismatches
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2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
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C;Species: Testudines gen. sp. (turtle)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
C;Accession: S63593
R;Kragelund, B.B.; Hojrup, P.; Skou Jensen, M.; Karlskov Schjerling, C.; Juul, E.; Knud: J. Mol. Biol. 256, 187-200, 1996
A;Title: Fast and one-step folding of closely and distantly related homologous proteins A;Reference number: S63592; MUID:96190960; PMID:8609609
A;Accession: S63593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Comment: This protein may be the endogenous ligand of the benzodiazepine C;Superfamily: endozepine; endozepine homology C;Keywords: acyl-CoA binding; antibate terrial; blocked amino end; intestine F;1-86/Product: endozepine #status experimental <MATI>F;18-74/Domain: endozepine homology <NDZ>F;32-86/Product: endozepine (32-86) #status experimental <MATI>
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A;Residues: 1-86 <CHE>
A;Residues: 1-86 <CHE>
R;Agerberth, B.; Boman, A.; Andersson, M.; Joernvall, H.; Mutt, V.; Boman, Eur. J. Biochem. 216, 623-629, 1993
Eur. J. Biochem. 216, 623-629, 1993
A;Title: Isolation of three antibacterial peptides from pig intestine: gast A;Reference number: S36839; MUID:93387315; PMID:8375398
S
                                                                                                                                                                                                         C; Keywords: acyl-CoA bindin F; 18-74/Domain: endozepine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acyl-coenzyme A-binding protein - turtle C; Species: Testudines gen. sp. (turtle)
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Eur. J. Biochem.
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C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endozepine -
                                                                                                                                                                                                                                          Superfamily: endozepine; endozepine; endozepine; endozepine; endozepine;
                                                                                                                                                                                                                                                                                                                   Residues: 1-86 <KRA>
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Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change
                                                                         Matches
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308 KGKAKWDA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50
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amino end (Ser) (probably acetylated)
                                                                                                                                                                                                                homology <NDZ>
                                                                                                                                                                                                                                                                              endozepine homology
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N;Contains: endozepine, short form
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1988 #sequence revision 30-Sep-1991 #text_change 22-Jun-1999
C;Date: 31-Dec-1988 #sequence revision 30-Sep-1991 #text_change 22-Jun-1999
C;Accession: A26448; S23127; A25832; A27886; A32944
R;Webb, N.R.; Rose, T.M.; Malik, N.; Marquardt, H.; Shoyab, M.; Todaro, G.J
DNA 6, 71-79, 1987
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R;Kragelund, B.B.; Hojrup, P.; Skou Jensen, M.; Karlskov Schjerling, C.; Juul, J. Mol. Biol. 256, 187-200, 1996

A;Title: Fast and one-step folding of closely and distantly related homologous A;Reference number: S63592; MUID:96190960; PMID:8609609
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R;Kragelund, B.B.; Hojrup, P.; Skou Jensen, M.; Karlskov Schjerling, C.; Juul, J. Mol. Biol. 256, 187-200, 1996

A;Title: Fast and one-step folding of closely and distantly related homologous A;Reference number: S63592; MUID:96190960; PMID:8609609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acyl-coenzyme A-binding protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: acya
F; 18-74/Domain:
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C;Species: Anas platyrhynchos (mallard)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
                                              A; Molecule type: mRNA
A; Residues: 1-87 <WEB>
                                                                                            A; Reference number: A; Accession: A26448
                                                                                                                  A;Title: Bovine and human cDNA sequences encoding a putative benzodiazepine receptor A;Reference number: A26448; MUID:87161236; PMID:2881742
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A;Cross-references: EMBL:M15886; NID:g162978; PIDN:AAA30495.1; R;Jensen, M.S.; Hojrup, P.; Rasmussen, J.T.; Knudsen, J.
                                                                                                                                                                                                                                                                                                    N; Alternate names: acyl-CoA-binding protein; diazepam-binding inhibitor
                                                                                                                                                                                                                                                                                                                               endozepine - bovine
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Keywords: acyl-CoA binding
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8; Conserv
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8; Conserv
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Pred. No.
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Biochem. J. 245, 857-861, 1987
A;Title: Amino acid sequence of acyl-CoA-binding protein from cow liver.
A;Reference number: A27886; MUID:88024142; PMID:3663196
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J. Biol. Chem. 261, 9727-9731, 1986
A;Title: Complete amino acid sequences of bovine and human endozepines: homology with A;Reference number: A25832; MUID:86278003; PMID:3525533
A;Accession: A25832
                                                                                                                                                                                                                                                                                                                                          R;Lihrmann, I.; Plaquevent, J.C.; Tostivint, H.; Raijmakers, R.; Tonon, M.C.; Conlon, J. Proc. Natll. Acad. Sci. U.S.A. 91, 6899-6903, 1994
A;Title: Frog diazepam-binding inhibitor: peptide sequence, cDNA cloning, and expression A;Reference number: A57711; MUID:94316605; PMID:8041717
A;Accession: A57711
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A;Title: Purification and characterization of variants of acyl-CoA-binding protein A;Reference number: S23127; MUID:92322005; PMID:1622397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diazepam-binding inhibitor - laughing frog
C;Species: Rana ridibunda (laughing frog)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 13-Aug-1999
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A;Accession: A32944
A;Molecule type: protein
A;Residues: 2-85 <BES>
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A;Title: Identification of des-(Gly-Ile)-endozepine as an effector of corticotropin-depe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Mikkelsen, J.; Hojrup, P.; Nielsen, P.F.; Roepstorff, P.; Knudsen, J.
Biochem J. 245, 857-861, 1987
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A; Residues: 1-88 <LIH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Experimental source: adrenal cortex; Comment: This protein may take part in the modulation; Superfamily: endozepine; endozepine homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Keywords: acetylated amino end; acyl-CoA binding;
?2-87/Product: endozepine #status experimental <MATS;
?2-85/Product: endozepine, short form #status experimental <MA2>;19-75/Domain: endozepine homology <NDZ>;2-85/Product: endozepine homology <NDZ>;2/Modified site: acetylated amino end (Ser) (in mature form) #s
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;Residues: 2-87 <MIK>
                                                                                                                                                                       ;Cross-references: GB:U09205; NID:g484097; PIDN:AAB60606.1; PID:g514280;Superfamily: endozepine; endozepine homology
;20-76/Domain: endozepine homology <NDZ>
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                                                      Local Similarity
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                                                         Conservative
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F;12-28/Domain: transmembrane #status predicted <TM1>
F;65-81/Domain: transmembrane #status predicted <TM2>
F;63-109/Domain: transmembrane #status predicted <TM3>
F;127-143/Domain: transmembrane #status predicted <TM4>
F;127-143/Domain: transmembrane #status predicted <TM4>
F;190-206/Domain: transmembrane #status predicted <TM5>
F;306-322/Domain: transmembrane #status predicted <TM6>
F;306-322/Domain: transmembrane #status predicted <TM7>
F;374-390/Domain: transmembrane #status predicted <TM9>
F;399-415/Domain: transmembrane #status predicted <TM9>
F;399-415/Domain: transmembrane #status predicted <TM9>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein At2g30590 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Datc: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Skelton, J.; Churcher, C.M. submitted to the EMBL Data Library, June 1995
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A;Cross-references: EMBL:Z49939; NID:g887599; PID:g887602; GSPDB:GN00013; MIPS:YMR221c
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A; Accession: S57589
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                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 13R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: SGD:S0004834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: MIPS: YMR221c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Experimental source: strain AB972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable membrane protein YMR221c -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE002093; NID:g1946360; PIDN:AAB63078.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-380 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Alternate names:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: C84710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local
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                                                                             Local
     240 YLVGYTLL 247
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8; Conserv
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8; Conserv
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hypothetical protein YM9959.03c
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                                                     Score 8; DB 2; Pred. No. 15; 0; Mismatches
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A;Molecule type: DNA
A;Residues: 1-547 <KUR>
A;Residues: 1-547 <KUR>
A;Cross-references: GB:AE006469; PIDN:AAK65262.1; PID:g14523713; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
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A;Experimental source: strain 1021, megaplasmid pSymA
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A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experi
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C;Species: Sinorhizobium meliloti
C;Dace: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: D95337
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Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows, Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 983-9889, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: D95337
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A; Residues: 1-508 < HAR>
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C;Accession: A43713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
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8; Conserv
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100.0%; Pred. No.
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No.
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o. 15;
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                                     A; Molecule type: protein
A; Residues: 1-86 < KRA>
C; Superfamily
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C;Superfamily: endozepine; en
C;Keywords: acyl-CoA binding
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RESULT 14
D95140
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A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: H97854
                                                                                                                                                                             acyl-coenzyme A-binding protein - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 28-Oct-1996 #sequence_revision
C;Accession: S65592
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A;Molecule type: DNA
A;Residues: 1-55 <KUR>
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A; Accession: S63592
                                     R;Kragelund, B.B.; Hojrup, P.; Skou Jensen, M.; Karlskov Schjerling, J. Mol. Biol. 256, 187-200, 1981 A;Tille: Fast and one-step folding of closely and distantly related ha;Reference number: S63592; MUID:96190960; PMID:8609609
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A;Experimental source: strain TIGR4
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Science 293, 498-506, 2001
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endozepine homology

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P;18-74/Domain: endozepine homology <NDZ>

Query Match
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 309 GKAKWDA 315
Db 51 GKAKWDA 57

Search completed: November 21, 2003, 14:24:33

Job time : 22 secs
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MEDLINE=88024142; PubMed=3663196; Mikkelsen J., Hoejrup P., Nielsen P.F., I "Amino acid sequence of acyl-CoA-binding Biochem. J. 245:857-861(1987).
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01-APR-1988 (Rel. 07, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ACyl-CoA-binding protein (ACBP) (Diazepam binding (Endozepine) (EP).
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Webb N.R., Rose T.
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NCBI_TaxID=9913;
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Mammalia; Eutheria;
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.M., Malik N., Marquardt H.,
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PIR; A26448; N2
PDB; 2ABD; 15-J
PDB; 1ACA; 30-A
PDB; 1HB8; 11-M
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J. Biomol. NMR 3:271-284(1993).

-i- FUNCTION: BINDS MEDIUM- AND LONG-CHAIN ACYL-COA ESTERS WITH VER' HIGH AFFINITY AND MAY FUNCTION AS AN INTRACELLULAR CARRIER OF ACYL-COA ESTERS. IT IS ALSO ABLE TO BEPACE DIAZEPIME (BZD) RECCUNITION SITE LOCATED ON THE GABA TYPE BENYZODIAZEPIME (BZD) RECCUNITION SITE THAT THIS PROTEIN ALSO ACTS
RECEPTOR. IT IS THEREFORE POSSIBLE THAT THIS PROTEIN ALSO ACTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jensen M.S., Hoejrup P., Rasmussen "Purification and characterization protein in the bovine liver.";
Biochem. J. 284:809-812(1992).
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ProDom; PD351532; Ac_coA_bind_prot;
PROSITE; PS00880; ACBP; 1.
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SIMILARITY: Belongs to the ACBP family.
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2ABD; 15-JUL-93.
1ACA; 30-ADL-94.
1HBB; 11-MAR-02.
rPro; IPR000582; Ac coA bind prot.
; PF00887; ACBP; 1.
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Biol. 226:1131-1141(1992)
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Best Local S
Matches 8
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_ACBP_CHICK
  proteins
J. Mol. B
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-i- FUNCTION: BINDS MEDIUM-AND LONG-CHAIN ACYL-COA ESTERS WITH VERY HICH AFFINITY AND MAY FUNCTION AS AN INTRACELLULAR CARRIER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Harderian gland;
MEDLINE=21240303; PubMed=11342056;
Cavagnari B.W., Sterin-Speziale N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chaétophractus villosus (South American armadillo).
Eukáryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Edentata; Dasypodidae; Chaetophractus.
                  Kragelund B.B., Hoejrup P., Jensen M.S., & Knudsen J., Poulsen F.M.; White the con-step folding of closely and proteins of a four-helix bundle family.";
                                                                                                                                                                                                                                                                     Acyli-CoA-binding protein (ACBP).
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                 Q9PRL8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=29080;
                                                                                                             MEDLINE=96190960; PubMed=8609609;
                                                                                                                                                                                                                              Archosauria;
                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                    16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transport; Lipid-binding; Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD351532; Ac coA bind prot; 1. PROSITE; PS00880; ACBP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00689; ACOABINDINGP
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Pfam; PF00887; ACBP; 1.
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                                                                                                                                                                                 TaxID=9031;
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1 (Rel. 40,
3 (Rel. 41,
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(Rel.
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Aves; Neognathae; Galliformes; Phasianidae; Phasiani
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to the ACBP family.
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Pred. No. 1.8;
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                                          related homologous
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Best Local :
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01-OCT-1989 (Rel.
16-OCT-2001 (Rel.
Acyl-CoA-binding p
(Endozepine) (EP)
                                -!- FUNCTION: DBI(32-86)
-!- SUBUNIT: Monomer.
-!- SIMILARITY: Belongs t
PIR; SO0805; NZPG.
HSSP; P07107; 1ACA.
                                                                                                                                                                                                                              MEDLINE=93387315; PubMed=8375398;
MEDLINE=93387315; PubMed=8375398;
MEDLINE=93887315; PubMed=8375398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transport;
SEQUENCE
                                                                                                                                                                                         "Isolation of three antibacterial peptides from pig intestine: gastric inhibitory polypeptide (7-42), diazepam-binding inhibitor (32-86) and a novel factor, peptide 3910.";
                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Intestine;
MEDLINE=89254787; PubMed=3289918;
Chen Z.W., Agerberth B., Gell K.,
Oestenson C.G., Efendic S., Barros
Joernvall H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00689; ACOABINDINGP
ProDom; PD351532; Ac coa bind
PROSITE; PS00880; ACBP; 1
                                                                                                                                                                                                                                                                                                                                    inhibitor, a polypeptide not common in intestinal tissues
                                                                                                                                                                                                                                                                                                                                      "Isolation and characterization of porcine diazepam-binding inhibitor, a polypeptide not only of cerebral occurrence but common in intestinal tissues and with effects on regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P12026
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HSSP; P07107; 1ACA.
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         InterPro; IPR000582;
Pfam; PF00887; ACBP;
                                                                                                                                                                                                                                                                                     SEQUENCE OF 32-86.
                                                                                                                                                                                                                                                                                                               Eur. J. Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                         insulin release.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: BINDS MEDIUM-AND LONG-CHAIN ACYL-COA ESTERS WITH HIGH AFFINITY AND MAY FUNCTION AS AN INTRACELLULAR CARRIER ACYL-COA ESTERS (BY SIMILARITY).

SIMILARITY: Belongs to the ACBP family.
                                                                                              FUNCTION: BINDS MEDIUM- AND LONG-CHAIN ACYL-COA ESTERS WITH VER HIGH AFFINITY AND MAY FUNCTION AS AN INTRACELLULAR CARRIER OF ACYL-COA ESTERS. IT IS ALSO ACE TO DISPLACE DIAZEPAM FROM THE BENZODIAZEPINE (BLD) RECOGNITION SITE LOCATED ON THE GABA TYPE RECEPTOR. IT IS THEREFORE POSSIBLE THAT THIS PROTEIN ALSO ACTS AS A NEUROPEPTIDE TO MODULATE THE ACTION OF THE GABA RECEPTOR.
                                                                                                                                                                              J. Biochem. 216:623-629(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308
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86 AA; 9645 MW;
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(Rel. 12, Last sequence update)
(Rel. 40, Last annotation update)
dding protein (ACBP) (Diazepam bin
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                                                                                       DBI (32-86)
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Rana ridibunda (Laughing frog) (Marsh frog).

Rana ridibunda (Chordata; Craniata; Vert

Subarvota; Metazoa; Chordata; Rana ridibunda (Rana ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RANRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P45883;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transport; Lipid-binding; Acetylation;
                                                                     PRINTS; PR00689; ACCABINDINGP.
ProDom; PD351532; Ac_coA_bind_prot; 1
PROSITE; PS00880; ACEP; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92319720; PubMed=1341880;
Malagon M., Vaudry H., Vallarino M., Gracia-Navarro F
"Distribution and characterization of endozepine-like
immunoreactivity in the central nervous system of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lihrmann I., Plaquevent J.-C., Tostivint P
Tonon M.-C., Conlon J.M., Vaudry H.;
"Frog diazepam-binding inhibitor: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acyl-CoA-binding protein homolog (ACBP) (Diaz homolog) (DBI)
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                                                                                                                                                                InterPro; IPR000582; Ac_coA_bind_prot.
Pfam; PF00887; ACBP; 1.
                                                                                                                                                                                                                                                PIR; A57711; A57711.
HSSP; P07107; 1ACA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptides 13:99-107(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                     EMBL; U09205; AAB60606.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94316605; PubMed=8041717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8406;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to the ACBP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: BRAIN. IS SELECTIVELY EXPRESSED IN GLIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: MAY PLAY IMPORTANT FUNCTIONS IN THE CONTROL OF BRAIN AND PITUITARY ACTIVITIES. MAY REGULATE GABA NEUROTRANSMISSION THROUGH A PARACRINE AND/OR AUTOCRINE MECHANISM. MAY NOT BIND ACYL-COA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANRI
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the brain.";
                                    Lipid-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acad.
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(Rel. 32, Last sequence update)
(Rel. 32, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sci. U.S.A. 91:6899-6903(1994).
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Pred. No. 1.8
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EBF128771E07A0F7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (32 - 86)
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Ranidae; Rana
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Q970Z3;
28-FEB-2003 (Rel.
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Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Ka Yoshizawa T., Tanaka T., Kidoh Y., Yamazaki J., Kushida N., Ogu Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.;
                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=JCM 10545 /
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                                                                                               PROSITE; PS01316; ATP P PHORIBOSYLTR; 1.
Histidine biosynthesis; Transferase; Glycosyltransferase;
Complete proteome.
                                                                                                                                                         HAMAP; MF_00079; -; 1.
InterPro; IPR001348; ATP_phspho_trans.
Pfam; PF01634; HisG; 1.
                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sulfolobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Crenarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sulfolobus
                                                                                                                                                                                                  EMBL; AP000986; BAB66530.1;
                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
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                                                                                                                                     rigrfams;
                                                                                                                                                  roDom;
                                                                                                                                                                                                                                                                                                                                  ATP + 5-phospho-alpha-D-ribose 1-diphosphate.

PATHWAY: Histidine biosynthesis; first step. Very important in tregulation of histidine metabolism.

SUBCELLULAR LOCATION: Cytoplasmic (By similarity)

SIMILARITY: BELONGS TO THE ATP PHOSPHORIBOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: 1-(5-phospho-D-ribosyl)-ATP + ATP + 5-phospho-alpha-D-ribose 1-diphosphate
                                                                                                                                                                                                                                                                                                                        LONG SUBFAMILY.
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            404
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                                                                                                                                    PD003516; ATP_phspho_s; TIGR00070; hisG; 1.
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8; Conserv
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8; Conserv
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283 AA;
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Pred. No
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Pred. No. 1.8;
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F6621EFCA12054BA CRC6
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                                                  No.
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                                                            DB
                                                DB 1;
4.9;
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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Li Y.-P.,
RA Langin-Hooper S., Lee A., Lucos J.S., Maiti R., Marziali A.,
Lin X., Liu S.X., Liu Z.A., Lucos J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Torium M.J., Town C.D.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SY81 ARATH STANDARD; PRT P59277; Q9C812; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequer 28-FEB-2003 (Rel. 41, Last annote Syntaxin 81 (AtSYP81).
SYP81 OR ATIG51740 OR F19C24.5.
                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=cv. Columbia;
MEDLINE=21016719; PubMed=11130712;
Theologis A., Ecker J.R., Palm C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
  SEQUENCE
                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feldmann K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 408:816-820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence and thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                 EMBL ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Full-length cDNA from Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                              TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                  nitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. FUNCTION: Vesicle trafficking protein that functions secretory pathway (By similarity).

SUBUNIT: Part of the t-SNARE complex (By similarity).

SUBUNIT: Part of the t-SNARE complex (By similarity).

SUBCELLULAR LOCATION: Type IV membrane protein (By similarity; BELONGS TO THE SYNTAXIN/EPHORPHIN FAMILY SIMILARITY; BELONGS TO THE SYNTAXIN/EPHORPHIN FAMILY CAUTION: Ref. 1 sequence differs from that shown due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                  gene model prediction.
                                                                                                                                   AC025294; AAG50888.1; ALT_SEQ.
AY086569; AAM63632.1;
TE; PS00914; SYNTAXIN; FALSE_NEG
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                                                                                                                     Protein transport;
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                  (POTENTIAL).
COILED COIL (POTENTIAL)
                                                          CYTOPLASMIC (POTENTIAL).
ANCHOR FOR TYPE IV MEMBRANE PROTEIN
                                                                                                                     Transmembrane;
  992C2B5F55B87B60
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                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
SSP consortium (Salk/Stanford/PGEC).";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Transcription factor. Interacts specifically with the
box (5'-(T)TGAC(C/T)-3'), a frequently occurring elicitor-
responsive cis-acting element (By similarity).
-!- SUBCELULAR LOCATION: Nuclear (Probable).
-!- INDUCTION: By salicylic acid.
-!- INDUCTION: By salicylic acid.
-!- SIMILARITY: Belongs to the WRKY group II-d family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C Fujii C.Y., Mason T.M., Bosman C.L., Barnstead M.E., Feldblyum Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WR21 ARATH
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                          EMBL; AF272747; AAK28441.1; -.
EMBL; U93215; AAB63078.1; -.
EMBL; BT000231; AAN15550.1; -.
EMBL; AY136441; AAM97106.1; -.
                                                                                                                                                                                                use by non-profit institumodified and this statement entities requires a license
                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yu D., Chen C., Chen Z.;
"Evidence for an important role of '
regulation of NPR1 gene expression.
Plant Cell 13:1527-1540(2001).
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                                                                                                                                        requires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
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21 (WRKY DNA-binding protein
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15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical 56.2 kDa protein in ERG8-UBP8 in
YMR221C OR YM9959.03C
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                                                                                                                                                                                                                                                                                                                               Time nucleotide XIII.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                         Nature 387:90-93(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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SMART; SM00220; S TKc; 1.

PROSITE; PS00018; EF HAND; 4.

PROSITE; PS00107; PROTEIN KINASE ATP; 1

PROSITE; PS00118; PROTEIN KINASE DOM; 1

PROSITE; PS50011; PROTEIN KINASE DOM; 1
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Pfam; PF00069; pkinase; 1.
ProDom; PD0000012; EF-hand; 2.
ProDom; PD000001; Prot kinase;
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INVOLVE CALCIUM AS A SECOND MESSENGER.

-:- ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.

-:- TISSUE SPECIFICITY: FOUND THROUGHOUT THE PLANT.

-:- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN SOYBEAN.

-:- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harper J.F., Sussman M.R., Schaller G.E., Charbonneau H., Harmon A.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
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Eukaryota; Viridiplantae;
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InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
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STRAIN=cv. Williams;
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SIMILARITY: Contains 4 EF-hand calcium-binding
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
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Evans E.W., Beach G.G., Wunderlich J., Harmon B.
"Isolation of antimicrobial peptides from avian
J. Leukoc. Biol. 56:661-665(1994).
-!- FUNCTION: BACTERICIDAL ACTIVITY; INHIBITS ST
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AMP2_MELGA
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                                                                                                                                                                                                                                                                                                                                EMBL; AF033338; AAC36054.1;
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MEDLINE=98418188; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9103;
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mon B.G., Jackwood M.W.;
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100.0%; Pred. No. 8.1;
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28-FEB-2003 (Rel.
28-FEB-2003 (Rel.
Acyl-CoA-binding (Endozepine) (EP)
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SEQUENCE
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STRAIN-Cross Broiler-6; TISSUB-Leukocyte;
MEDLINE-94200386; PubMed-8150085;
HARWIG S.S.L., Swiderek K.M., Kokryakov V.N., Tan L.,
Panyutich E.A., Aleshina G.M., Shamova O.V., Lehrer R.
"Gallinacins: cysteine-rich antimicrobial peptides of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercial
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Kragelund B.B., Hoejrup P., Jensen M.S., S
Knudsen J., Poulsen F.M.;
"Fast and one-step folding of closely and
proteins of a four-helix bundle family.";
                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                           MEDLINE=96190960; PubMed=8609609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibiotic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98418188;
                                                                                                                                                                 NCBI_TaxID=9615;
                                                                                                                                                                                                                                            Canis familiaris (Dog).
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AND L.MONOCYTOGENES EGD BUT NOT C.ALBICANS.
SUBCELLULAR LOCATION: Cyroplasmic granules.
SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY
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29:283-289(1998).
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                                                                   Schjerling C.K., Juul E.,
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MBL outstation -
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Best Local (
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P07108; P08869;
P07108; P08869;
O1-APR-1988 (Rel. 07, Created)
O1-NOV-1988 (Rel. 09, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Acyl-CoA-binding protein (ACBP) (Diazepam binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD RES
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INIT_MET
MOD_RES
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIGH AFFINITY AND MAY FUNCTION AN ACYL-COA ESTERS.
-!- SUBUNIT: Monomer (By similarity)
-!- SIMILARITY: Belongs to the ACBP PIR; $63592; $63592.
HSSP; P07107; 1ACA.
                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=87016986; PubMed=3020548;
Gray P.W., Glaister D., Seeburg P.H., Guidotti A.,

"Cloning and expression of cDNA for human diazepam
a natural ligand of an allosteric regulatory site c
aminobutyric acid type A receptor.";

Proc. Natl. Acad. Sci. U.S.A. 83:7547-7551(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=87161236; Publ
Webb N.R., Rose T.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
MEDLINE=86278003; PubMed=3525533;
Marquardt H., Todaro G.J., Shoyab M.;
Marquardt H., Todaro Gequences of bovine and human
"Complete amino acid sequences of bovine and human
Homology with rat diazepam binding inhibitor.";
J. Biol. Chem. 261:9727-9731(1986).
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Mammalia; Eutheria;
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                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                           "Bovine and human cDNA sequences encoding receptor ligand.";
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6:71-79(1987).
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BINDS MEDIUM-AND LONG-CHAIN ACYL-COA ESTERS WITH
MAY FUNCTION AS AN INTRACELLULAR CARRIER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. J. 306:327-330(1995).

-i. FUNCTION: BINDS MEDIUM- AND LONG-CHAIN ACYL-COA ESTERS WITH VERHIGH AFTENITY AND MAY FUNCTION AS AN INTRACELLULAR CARRIER OF ACYL-COA ESTERS. IT IS ALSO ABLE TO DISPLACE DIAZEPAM FROM THE BENEZODIAZEPINE (BZD) RECOGNITION SITE LOCATED ON THE GABA TYPE RECEPTOR. IT IS THEREFORE POSSIBLE THAT THIS PROTEIN ALSO ACTS A NEUROPEPTIDE TO MODULATE THE ACTION OF THE GABA RECEPTOR.

-i. SUBUNIT: MONOMER:
-i. ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=a 1; Synonyms=Short;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                          SEQUENCE
                                                                                                                                                                                                                                                           GO; GO:0008025; F:diazepam-binding inhibitor activity; GO; GO:0005102; F:receptor binding activity; TAS. InterPro; IPR000582; AC combind_prot.
Pfam; PF00887; ACBP; 1.
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HSSP; P07107; 1ACA.
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IsoId=P07108-2; Sequence=VSP_000068;
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Score 7; DB 1
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Copyright (c) 1993 - 2003 Compugen Ltd.
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INFORMATION FOR SEQ ID NO:
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LENGTH: 86 amino acids
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	
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1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	
257	203	188	188	188	188	188	188	187	104	96	96	77	77	77	77	64	64	
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US-09-252-991A-23705	US-09-134-001C-3145	US-08-149-223A-20	US-08-458-731-20	US-08-480-150A-20	US-08-484-596A-20	US-08-484-158B-20	US-08-484-993B-20	US-09-252-991A-29325	US-08-700-626-3	US-09-300-008B-55	US-08-700-626-4	PCT-US92-06412-57	US-08-823-771-75	US-08-474-633A-75	US-08-182-175A-57	US-09-351-657A-8	US-09-351-657A-4	
Sequence 23705, A	Sequence 3145, Ap	20,	20,	æ	e 20,	Sequence 20, Appl	20,	Sequence 29325, A	Sequence 3, Appli	Sequence 55, Appl	Sequence 4, Appli	Sequence 57, Appl	75,	Sequence 75, Appl	e 57,	Sequence 8, Appli	Sequence 4, Appli	

ALIGNMENTS

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APPLICATION NUMBER: US/08/700,626
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGERENCE/DOCKET NUMBER: PF-0115
REFERENCE/DOCKET NUMBER: PF-0115 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL HUMAN DBI/ACBP-LIKE PROTEIN NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Au-Young, Janice
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Incyte Pharmaceuticals, Inc
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DB 1;
                       Length 86;
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Gaps

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Query Match
Best Local Similarity
Marches 8; Conserve
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                                                                                                                US-07-951-715A-25
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION BOO
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
AFTORNEY/AGENT INFORMATION:
NAME: Spruill, W. MULTRAY
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                TELEFAX: (919)541-8689
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 32,943
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEPAX: (919)541-8615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                        OLECULE TYPE:
                                                                                                                           LOCATION: 1..463
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                          LENGTH: 463 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive CITY: Hawthorne
                                                                                                                                                                                  NAME/KEY: Protein
                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                            ropology:
 394 ERQAARLI 401
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Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
                                     Conservative
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Merlin, Ellie J.
Launis, Karen L.
                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                      : protein
                                                     1.6%;
100.0%;
                                                                                                                             /note= "protein sequence
soybean CDPK as shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steven J
                                                                                                                                                                                                                                                                                                                                                     25:
                                                     Score 8; I
                                     0; Mismatches
                                                          DB 1;
o. 17;
                                                                      Length 463;
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n Figure 34."
                                     0; Indels
                                     <u>,</u>
                                     Gaps
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RESULT 3
US-08-459-448A-25
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                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                 TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Suttie, Janet L. TITLE OF INVENTION: SYNTHET TITLE OF INVENTION: INSECTI NUMBER OF SEQUENCES: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT
APPLICANT
                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: No. 5859336artis Corporation STREET: Patent & Trademark Dept., 520 White Plains STREET: Rd., POB 2005
                                                                                                                          TOPOLOGY:
                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                  ENGTH:
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                                                                                                                                                                                463 amino acids
                                                                                                                       linear
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Dunder, Erik M.
Pace, Gary M.
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Merlin, Ellis J.
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                                                                                     .. protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
   /note= "protein sequence for
soybean CDPK as shown in Figure 34."
                                                                                                                                                                                                                                                                            40403
BER: CGC 1577/CIP/DIV4
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Length 463; 0; Indels

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rothst
APPLICANT: Bowman
APPLICANT: Dawson,
APPLICANT: Dawson,
APPLICANT: Daveson,
APPLICANT: Statele,
TILE OF INVENTION:
TILE OF SEQUENCE:
TRESPON:
                                                                                                                                           TELEFAX: (919)541-868
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tent No.
                                                                                                                                                                                               APPLICATION NOTICE 1991
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REGISTRATION NUMBER: CGC 1577/CIP/DIV3
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMBER: US/08/459,595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING APPLICATION NUMBER: US 07/772,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: CG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
                             POTHETICAL:
                                                                            TYPE: amino acid
STRANDEDNESS: si
NAME/KEY:
                                                                                                                                                                        TELEPHONE:
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                                                               COPOLOGY:
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                                                                                                             ENGTH:
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6018104
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                                                                                                           463 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: No. 6018104artis Corporation
Patent & Trademark Dept., 520 White Plains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                (919)541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pace, Gary M.
Suttie, Janet L.
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Protein
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Dunder, Erik M.
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Launis, Karen L.
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                                                             linear
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                           .: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ewis,
                                                                                                                                                                              (919)541-8582
                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stephen V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kelly S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.6%; Score 8; DB 2;
100.0%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                               25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 02-UN-1995
APPLICATION NUMBER: US 07/
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 04-CCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: MAGGET TECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No.
                                            NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATIBLE

COMPUTER: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,504B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: NC
COUNTRY: US
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity es 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394 ERQAARLI 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T: Suttie, Janet L
INVENTION: SYNTHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3E: No. 6075185artis Corporation
3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08459504B
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Dunder, Erik M.
Pace, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bowman, Cindy G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rothstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Merlin, Ellis J.
Launis, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Desai, Nalini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wright, Martha S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vance C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.6%; Score 8; DB:
100.0%; Pred. No. 17,
ive 0; Mismatches
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                                                                                                                                                                                             US 07/772,027
                                                                                                                                                                                                                                                                          US 08/459,595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steven J
                                                                                                                                                                                                                                             07/951,715
                                                                                                             CGC1577/CIP/DIV
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Query Match
Best Local Similarity
Matches 8; Conserve
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GENERAL INFORMATION:
                                                                                             INFORMATION FOR SEQ ID NO: /note= "protein sequence for soybean CDPK as shown in Figure 34."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-7un-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..463
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Protein
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                                                                                                                               NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEPHONE: (919)541-8587
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 27709
STRANDEDNESS: single TOPOLOGY: linear
                                        TYPE: amino acid
                                                         ENGTH: 463 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Koziel, Michael G
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Lewis, Kelly S
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soybean CDPK as shown in Figure 34."
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Mismatches
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NAME/KEY: Protein; LOCATION: 1..463; SEQUENCE DESCRIPTION: SEQ ID NO: 25: US-08-459-444-25
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Best Local Similarity 100.0%;
                                                                          TELECHONE: (919)541-8587
TELEPHAX: (919)541-8689
INFORMATION FOR SEQ ID NO: /note= "protein sequence for soybean CDPK as shown in Figure 34."
                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/547,422
FILING DATE: 11-Apr-2000
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/547,422
FILING DATE: 11-Apr-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                 NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research,
STREET: 3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO FEATURE:
                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SYNTHETIC DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Koziel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 ERQAARLI 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8;
LENGTH: 463 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
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Lewis, Kelly S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Michael G
Nalini M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INSECTICIDAL ACTIVITY
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ACTIVITY IN MAIZE
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TYPE: PRT
ORGANISM: Pinus radiata
US-09-228-986-73
                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-182-175A-4
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                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 55592
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                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Saverio Carl Falc

APPLICANT: Sharon J. Keeler

APPLICANT: Janet A. Rice

APPLICANT: Janet A. Synthet:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Compositions Isolated from Plant Cells TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling FILE REFERENCE: 11000/1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Strabala, Timothy APPLICANT: Nieuwenhuizen, Niels
APPLICATION NUMBER: UPPLICATION DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
                                                                             COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System,
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                             CITY: Wilmington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.0%; es 8; Conservative
                                                                                                                                                                                 ZIP: 19898
                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                 Delaware
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                                                                                                                                                                                                                                                                                                                                                             Saverio Carl Falco
                                                                                                                                                                                                                                                                                             Synthetic Storage Proteins with Defined Structure Containing: 113
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100.0%; Pred. No.
   07/743,006
                                                                US/08/182,175A
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                                                                                                                 6.0
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RESULT 10
US-08-182-175A-49
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TELEFAX: (302) 892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
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Patent No. 555522...
Patent No. 555522...
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Patent No. 555522...
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Patent No. 555522...
Patent No. 555522...
Patent No. 555522...
Patent No. 55562...
Patent No. 55562...
Patent No. 55662...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local :
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TELEX: 835420
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
COMPUTER: Macintosh System,
OPERATING SYSTEM: Macintosh System,
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1007 Mar)
CITY: Wilmington
STATE: Delaware
                                                                                                                             TELEPHONE: (302) 892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 7; DB : 100.0%; Pred. No. 13 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= name
/note= "(SSP
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ER: BB-1031
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5. 13;
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E. I. DU PONT DE NEMOURS AND

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-182-175A-49
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Best Local Similarity
Marches 7; Conserva
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                                             US-08-474-633A-58
                                                               RESULT 12
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Best Local Similarity
""tches 7; Conserv
                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amin
Type:
Sequence 58, Application US/08474633A Patent No. 5773691 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/182, FILING DATE: CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/743,006 FILING DATE: 9 August 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 9 August 19 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy Disk
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OPERATING SYSTEM: Macintosh System,
SOFTWARE: Microsoft Word, 4.0
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CITY: Wilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                         LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
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1007 Market Street
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                                                                                                                                                                                                                                                                                                                                                                                        (302) 892-7949
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                                                                                                                                                                          1.4%; Score 7; DB : llarity 100.0%; Pred. No. 13 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                             unknown
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o. 13;
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US-08-474-633A-73
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                                                                                                                                                                                                                                                       Patent No. 5773691
GENERAL INFORMATION:
APPLICANT: E. I.
                                                                                                                                                                                                                                                                                           Sequence 73, Application US/08474633A Patent No. 5773691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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INFORMATION FOR SEQ ID NO:
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APPLICANT: COMPANY
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                   APPLICANT: COMPANY
TITLE OF INVENTION: N
TITLE OF INVENTION: N
TITLE OF INVENTION: 1
TITLE OF INVENTION: C
TITLE OF INVENTION: C
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,633A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                     CORRESPONDENCE ADDRESS:
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                              CITY: WILMINGTON STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.0%;
nes 7; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
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CITY: WILMINGTON
ZIP: 19898
                                                                                  ADDRESSEE: E.
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ADDRESSEE: AND COMPANY
                                                                   STREET:
                COUNTRY:
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Y: U.S.A.
                                                                     1007 MARKET STREET
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                U.S.A.
                                                                                       AND COMPANY
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                                                                                                   DU PONT DE NEMOURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DU PONT DE NEMOURS
                                                                                                                                                   METHODS FOR INCREASING INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METHODS FOR INCREASING INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF PLANTS
                                                                                                                                                                                                                           CHIMERIC GENES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHIMERIC GENES AND
                                                                                                                                       107
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100.0%; Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 28;
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COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK

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US-08-823-771-58
; Sequence 58, Application in the sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequence 58, Sequen
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTÖRNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/474,633

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: BARBARA C. SIEGELL

REGISTRATION NUMBER: 30,684

REGISTRATION NUMBER: BB-1037-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: 302-992-4931
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Local Similarity 100.0%; Pred. No. 13;
les 7; Conservative 0; Mismatches
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TOPOLOGY: unk
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: CHIMERIC GENES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 EKLKKME 487
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/823,771
FILING DATE: 24-Mar-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1007 MARKET STREET CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08823771
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Query Match
Best Local Similarity
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                                                                              ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-08-823-771-73
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Best Local Similarity
Matches 7; Conserv
                                      Query Match
                                                                                                                                                       TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION NUMBER: US/08/823,771
FILING DATE: 24-Mar-1997
CLASSIFICATION NUMBER: 08/474,633
APPLICATION NUMBER: 08/474,633
APPLICATION NUMBER: 08/474,633
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APPLICATION NUMBER: 08/474,633
APPLICATION NUMBER: 08/474,633
APPLICATION NUMBER: 08/474,633
APPLICATION NUMBER: 08/474,633
APPLICATION NUMBER: 08/474,633
ATTORNEY/AGENT UNDERS: 08-4931
TELEPRONE: 302-992-4931
TELEPRONE: 302-992-4931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: E. I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 EKLKKME 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1007 MARKET STREET CITY: WILMINGTON STATE: DELAWARE
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AND COMPANY
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                      1.4%; Score 7; I
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 7; DB 4
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0; Mismatches
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                    DB 4;
o. 13;
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481 EKLKKME 487

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3 EKLKKME 9

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Search completed: November 21, 2003, 14:25:05 Job time : 21 secs

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Minimum DB
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Cgn12_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ Cgn12_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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/ Cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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/ Cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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                         US-09-987-108-3

US-09-987-108-3

US-09-987-108-7

US-09-987-108-8

US-09-987-108-9

US-09-987-108-9

US-09-988-462-25

US-09-988-462-25

US-09-988-462-25

US-10-1014-464-73

US-10-1014-604-26
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US-09-864-761-33415
US-09-859-101-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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2469.624 Million cell updates/sec
                                                             Sequence 6, Appli
Sequence 29742, A
Sequence 33415, A
Sequence 5, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 7294, Appl
Sequence 7294, Appl
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US-09-938-803-6

Sequence 6, Application US Patent No. US20020076762A1

Application US/09938803

## ALIGNMENTS

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SOFTWARE: PERL Program

SEQ ID NO 6

LENGTH: 487

TYPE: PRT
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte Clone 1928920
US-09-938-803-6
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                                                                                                                 Matches 487;
                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/938,803
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 09/311,894
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Reddy, Roopa
APPLICANT: Baughn, Mariah R.
APPLICANT: Yang, Junming
APPLICANT: Azimzai, Yalda
TITLE OF INVENTION: FULL-LENGTH EXPRESSED GENETIC MARKERS
FILE REFERENCE: PF-0695 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
61 YLFYKETYLIHLFHTFTGLSIAYFNFGNQLYHSLLCIVLQFLILRLMGRTITAVLTTFCF 120
                                                               1 MASSAEGDEGTVVALAGVLQSGFQELSLNKLATSLGASEQALRLIISIFLGYPFALFYRH
                                       MASSAEGDEGTVVALAGVLQSGFQELSLNKLATSLGASEQALRLIISIFLGYPFALFYRH
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Lal, Preeti
                                                                                                                   Conservative
                                                                                                                                     100.0%; Score 487; 100.0%; Pred. No. 0;
                                                                                                           0,
                                                                                                                   Mismatches
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                                                                                                                                                       9; Length 487;
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US-10-029-386-29742
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Best Local S
Matches 56
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                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: MAP TO CONTINUE TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TO
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APPLICANT: Hanzel, David K.
APPLICANT: HANZEL DAVID K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: ABOMICA X-2
CURRENT FILING DATE: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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N
                                                                                                                                                                           Similarity
EGVCILTGLGFNGFEEKGKAKWDACANMKVWLFETNPRFTGTIASFNINTNAWVAR 57
                                 EGVCILTGLGFNGFEEKGKAKWDACANMKVWLFETNPRFTGTIASFNINTNAWVAR 347
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                                                                                                                                             Conservative
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NN: EXPRESSED IN PLACENTA, SIGNAL = 3.7

NN: EXPRESSED IN LUNG, SIGNAL = 3.7

NN: EXPRESSED IN HEARIN, SIGNAL = 3.5

NN: EXPRESSED IN HEARIN, SIGNAL = 4.4

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 6.8

NN: EXPRESSED IN BONE MARROW, SIGNAL = 3.1

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 3.6

NN: EXPRESSED IN HELA, SIGNAL = 4.6

NN: EXPRESSED IN HELA, SIGNAL = 4.5

NN: EXPRESSED IN HELA, SIGNAL = 4.5
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Pred. No.
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US-09-864-761-33415
US-09-864-761-33415
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PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR PRILING DATE: 2000-09-27
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
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APPLICANT: Penn, Sharron G
APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33415, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Annomax SEQ ID NO 33415
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                            OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
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                    N: MAP TO ACO06512:12

N: EXPRESSED IN LING, SIGNAL = 5.5

N: EXPRESSED IN BRAIN, SIGNAL = 2.2

N: EXPRESSED IN PLACENTA, SIGNAL = 6.6

N: EXPRESSED IN PLACENTA, SIGNAL = 6.6

N: EXPRESSED IN HELLOO, SIGNAL = 3.6

N: EXPRESSED IN HELLA, SIGNAL = 3.5

N: EXPRESSED IN HELA, SIGNAL = 3.5

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6

N: EXPRESSED IN BIGNAL = 5.9

N: EXPRESSED IN BIGNAL = 5.9

N: EXPRESSED IN BIGNAL = 5.9

N: EXPRESSED IN HELA, SIGNAL = 5.9

N: EXPRESSED IN HELA, SIGNAL = 5.9

N: EXPRESSED IN HEART, SIGNAL = 2

N: EXPRESSED IN HEART, SIGNAL = 3.00e

N: EXPRESSED IN HEART, SIGNAL = 3.00e

N: EXPRESSED IN HEART, SIGNAL = 3.00e

N: EXPRESSED IN HEART, SIGNAL = 3.00e
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BONE MARROW, SIGNAL = 1
HBL100, SIGNAL = 6.6
FETAL LIVER, SIGNAL =
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US-09-859-101-5
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Patent No. US20020068825A1
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
Hillman, Jennifer L.
Goli, Surya K.
     GENERAL INFORMATION:
APPLICANT: KNUDSEN, Jens
APPLICANT: WADDM, Maiken C.T.
APPLICANT: VILLADSEN, Jens
                                                                            Sequence 1, Application US/09987108 Patent No. US20020142347A1
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TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                              CLONE: 118275
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/859,101
FILING DATE: 14-May-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptid
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL HUMAN DBI/ACBP-LIKE PROTEIN NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                     308 KGKAKWDA 315
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TYPE: amino acid
STRANDEDNESS: single
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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STREET: 3174 Porter Drive
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100.0%; Pr
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Sequence 7, Application US/09987108
Patent No. US20020142347A1
GENERAL INFORMATION:
APPLICANT: KNUDSEN, Jens
APPLICANT: WADUM, Maiken C.T.
APPLICANT: VILLADSEN, Jens
APPLICANT: NEERGAARD, Thomas B.F.
TITLE OF INVENTION: BIOSENSOR
FILE REFERENCE: KNUDSENIA
CURRENT APPLICATION NUMBER: US/09/987,108
CURRENT FILING DATE: 2001-11-13
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; TYPE: PRT
; ORGANISM: Bos taurus
US-09-987-108-1
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LENGTH: 86
TYPE: PRT
ORGANISM: Sus s
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Matches 8
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APPLICANT: WADUM, Maiken C.T.
APPLICANT: VILLADSEN, Jens
APPLICANT: NEERGAARD, Thomas
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see 8; Conserv
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Sequence 3, Application US/09987108 Patent No. US20020142347A1
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CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/262,366
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: DK PA2000 01638
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                            PRIOR APPLICATION NUMBER: DK PA2000 01638 PRIOR FILING DATE: 2000-11-10 NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                              APPLICANT: NEERGAARD, Thomas B.F.
TITLE OF INVENTION: BIOSENSOR
FILE REFERENCE: KUUDSENIA
CURRENT APPLICATION NUMBER: US/09/987,108
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/262,366
PRIOR FILING DATE: 2001-01-19
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Thomas B.F.
                1.6%; Score 8; 1
100.0%; Pred. No.
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Pred. No.
 Mismatches
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PRIOR APPLICATION NUMBER: US 60/262,366
PRIOR APPLICATION NUMBER: US 60/262,366
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2000-11-10
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: KNUDSEN, Jens
APPLICANT: WADDUM, Maiken C.T.
APPLICANT: VILLADSEN, Jens
APPLICANT: NEERGAARD, Thomas B.F.
TITLE OF INVENTION: BIOSENSOR
FILE REFERENCE: KNUDSENIA
CURRENT APPLICATION NUMBER: US/09/987,108
CURRENT APPLICATION 2001-11.13
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Best Local Similarity
Marches 8; Conserve
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; TYPE: PRT
; ORGANISM: Anas platyrhynchos
US-09-987-108-8
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                                                                                                                                                                                                                                                    Sequence 9, Application US/09987108 Patent No. US20020142347A1 GENERAL INFORMATION:
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              CURRENT APPLICATION NUMBER: US/09/987,108
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/262,366
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: DK PA2000 01638
PRIOR FILING DATE: 2000-11-10
                                                                                                                               APPLICANT: KNUDSEN, Jens
APPLICANT: WADUM, Maiken C.T.
APPLICANT: VILLADSEN, Jens
APPLICANT: NEERGAARD, Thomas B.F.
TITLE OF INVENTION: BIOSENSOR
FILE REFERENCE: KNUDSENIA
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PRIOR APPLICATION NUMBER: DK PA2000 01638
PRIOR FILING DATE: 2000-11-10
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NUMBER OF SEQ ID NOS:
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)S: 38
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100.0%; Pred. No.
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US-09-988-462-25
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Best Local Similarity 100.0%;
Matches 8; Conservative (
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SEQ ID NO 20
LENGTH: 86
TYPE: PRT
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SEQ ID NO 9
LENGTH: 86
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APPLICANT: WADUM, Maiken C.T.
APPLICANT: VILLADSEN, Jens
APPLICANT: NEERGAARD, Thomas B.F.
TITLE OF INVENTION: BIOSENSOR
FILE REFERENCE: KNUDSENIA
CURRENT APPLICATION NUMBER: US/09/987,108
CURRENT FILING DATE: 2001-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/262,366
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: DK PA2000 01638
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Rana sp.
                                                                                                                        Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Marcha S.
Merlin, Ellis J.
Launis, Karen L.
TITLE OF INVENTION: SYNTHETIC I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.0%;
                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Biotechnology, Inc
STREET: 3054 Cornwallis Road
                                                                                        NUMBER OF SEQUENCES: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 KGKAKWDA 315
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CITY: Research
STATE: NC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                            Koziel, Michael G
                                                                                                                                                                                                                                                                                       Desai, Nalini
                                                                                                                                                                                                                                                                        Lewis, Kelly S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.6%; Score 8; DB 1
100.0%; Pred. No. 11;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.6%; Score 8; DB 10; Length 86; 100.0%; Pred. No. 11;
                                                                                                         SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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; NAME/KEY: Protein
; LOCATION: 1..463
; OTHER INFORMATION: /note= "protein sequence for
soybean CDPK as shown in Figure 34."
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-988-462-25
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US-10-032-585-7294
                                                   APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 7294
                                                                                                                                                                                                                                                                                                               Sequence 7294, Application US/10032585 Publication No. US20030180953A1 GENERAL INFORMATION:
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Matches 8; Conserv
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TELEPAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                       TYPE: PRT
               ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 463 amino acids
TYPE: amino acid.
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 ERQAARLI 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-No. US20030046726A1-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.6%; Score 8; DB larity 100.0%; Pred. No. 50 Conservative 0; Mismatches
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                                                                             US-09-814-604-26
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                                                                                                             APPLICANT: Klein, Elliott S.
APPLICANT: Chandraratna Roshantha A.
APPLICANT: Chandraratna Roshantha A.
TITLE OF INVENTION: Methods of Detecting Dissociated Nuclear
TITLE OF INVENTION: Hormone Receptor Ligands
FILE REFERENCE: P-AR 4528
CURRENT FLILORION NUMBER: US/09/814,604
CURRENT FLING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 20
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                               Sequence 26, Application US/09814604 Publication No. US20030003517A1 GENERAL INFORMATION:
   Matches
                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 73, Application US/10101464A Publication No. US20030046728A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Compositions Isolated from Plant Cells TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR PILING DATE: 2000-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 989
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PRIOR FILING DATE: 2000-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/162,866 PRIOR FILING DATE: 1999-11-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Strabala, Timothy APPLICANT: Nieuwenhuizen, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Higgins, Colleen M.
                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 947
TYPE: PRT
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Local Similarity 100.0%;
les 8; Conservation
 Local Similarity
les 7; Conserv
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nes 8; Conservative (
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   Conservative
                     100.0%;
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100.0%; Pred. No. 64;
ive 0; Mismatches
; Score 7; DB 1
%; Pred. No. 26;
0; Mismatches
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                     DB 11;
o. 26;
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o. 64;
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5. 95;
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                                     Length 20;
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 Indels
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76 FTGLSIA 82

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8 FTGLSIA 14

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US-09-922-226-12

i Sequence 12, Application US/0992226

publication No. US20030077664A1

i General Information:
APPLICANT: Klao, Jia-Hao
APPLICANT: Klao, Joi-Hao
APPLICANT: Klao, Joi-Hao
APPLICANT: Klao, Joi-Hao
APPLICANT: Klao, Joi-Hao
APPLICANT: Chandraratna, Roshantha A.
TITLE OF INVENTION: Methods of Screening For Compounds That
TITLE OF INVENTION: Methods of Screening For Activity

FILE REFERENCE: P-AR 4681

CURRENT APPLICATION NUMBER: US/09/922,226

CURRENT FILING DATE: 2002-01-09

PRIOR APPLICATION MUMBER: US/09/922,226

CURRENT FILING DATE: 2001-04-18

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 12

LENGTH: 20

TYPE: PRT

US-09-922-226-12

Query Match
Best Local Similarity 100.0%; Pred. No. 26;
Matches: 7; Conservative 0; Mismatches 0; Indels 0; Gaps

Oy

76 FTGLSA 82

Db 8 FTGLSIA 82

Db 1 FTGLSIA 82

Db 1 FTGLSIA 14

Search completed: November 21, 2003, 14:29:34
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
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## SUMMARIES

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## ALIGNMENTS

TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX048067	RESULT 1
Yang, J., Azimzai, Y., Lu, D.A., Au-Young, J. and Shih, L.L. Full-length molecules expressed in human tissues	Yue, H., Tang, Y.T., Lal, P., Reddy, R., Batra, S., Baughn, M.R.,		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)		AX048067.1 GI:11876890	AX048067	Sequence 61 from Patent WO0070047.	AX048067 2273 bp DNA linear PAT 15-DEC-2000		

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Query Match Best Local Matches 225  Qy 1 Db 7 Qy 60 Db 67	CDS BASE COUNT	AXO73570 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	Qy Db Oy Oy Oy Oy Oy Oy Oy Oy Oy Oy Oy Oy Oy
y Match y Match y Match Local Similarity 99.8%; Pred. No. 0; Local Similarity 99.8%; Pred. No. 0; hes 2254; Conservative 0; Mismatches 3; Indels 1; Gaps 1; l GGGGTGAAGCGATA-CGTTTTGCCCGCATTCGGGGCGCGCGCACTGGGGGGTCCCTGT 59	/mol type="genomic DNA" /db_xref="texon:9606"  851548  851548 /note="unnamed protein product" /codon start=1 /protein_id="CAC28402.1" /brotein_id="CAC28402.1" /db_xref="G:12709985" /translation="MASSAEGDEGTVVALAGVIQSGFQELSLNKLATSLGASEQALRL IISIFLGYPFALFYRHYLFYKETYLIHLFHTFTGLSIAYENFGNQLYHSLLGIVLQFL IIRLMGRTITANUTTFCCPQMAYLLAGYYYTATGNYDIKWTMPHCVLTLKLLGLAUDYF DGGKDQNSLSSEQQKYAIRGVPSLLEVAGFSYFYGAFLVGPQFSMNHYMKLVQGELID IPKKINSI IPALKRLSIGLFYLVGYTILSPHITEDYLLTEDYDNHPFWFRCMYMLIW GKFULYKYYTCMLYTGKYCLITGLGFNGFSEKGKAKMDACANMKVWLFETNPRFTGTI ASFNINTNAWVARYIFKRLKFLCNKELSGGLSLLFLALWHGLHSGYLVCFGNBETLIVI VERQAARLIGESPTLSKLAAITYLQPFYYLVQQTIHWLFMGYSMTAFCLFTWDKWLKV YKSIYFLGHIFFLSLLFILPYIHKAMVPRKEKLKKME"  482 a 629 c 550 g 603 t	AX073570  N Sequence 22 f. AX073570.1 G. AX073570.1 G. Homo sapiens M Homo sapiens Eukaryota, Mel Mammalia; Eutl 1 Kato, S. and K. Human proteins proteins Patent: WO 010 SAGAMI CHEMIC SAGAMI CHEMIC SAGAMI CHEMIC LOCAL	1981 GCGTGAGCCACCGTGCCCGGCCCAAAGGGGAAACTCTTGTGGGAGGAGGAGAGGGGCTCA 2040 1981 GCGTGAGCCACCGTGCCCGGCCCAAAGGGGGAAACTCTTGTGGGAGGAGCAGAGGGGCTCA 2040 2041 CATCTCCCCTCTGATTCCCCCATGCACATTGCCTTATCTCTCCCCATCTAGCCAGGAATC 2100 2041 CATCTCCCCTCTGATTCCCCCATGCACATTGCCTTATCTCTCCCCATCTAGCCAGGAATC 2100 2041 CATCTCCCCTCTGATTCCCCCATGCACATTGCCTTATCTCTCCCCATCTAGCCAGGAATC 2100 2101 TATTGTGTTTTTCTTCTGCCAATTTACTATGATTGTGTCTGCCGCTACCACCACCCC 2160 2101 TATTGTGTTTTTCTTCTGCCAATTTACTATGATTGTGCCGCTACCACCACCCCC 2160 2101 TATTGTGTTTTTCTTCTGCCAATTTACTATGATTGTTGCCGCTACCACCACCCCC 2160 2101 CCCATGGGGGGGGGAGAGGGGTGCAAGGCCCTGCCTGCTCTACCACCACCACCCCC 2160 2161 CCCATGGGGGGGTGGAAGAGGGGTGCAAGGCCCTGCCCCCCCC
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Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:s81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction; Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB, annotation: HRI and RAB.
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Homo sapiens (human)
Homo sapiens
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Isogai,T. and Yamamoto,J.
Direct Submission
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RESULT 4 BC000664 BC000664 BC000664 BC000664 BC000664 BC000664 BC000664 CCDNA clone MGC:1311 IMAGE:3349388), complete cds. BC000664 VERSION BC000664.1 GI:12653756 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 2058)	Db 16.05 TCCHITACTTCCTCTCACCTCTACGTGGGACALATTAGGCTTAAATCCATTACCATAAATCCATTACCATAATTCCATTACCATAATTCCATTACCATAAATCCATTACCATACATACCATTA

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REFERENCE
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
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Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
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Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
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human and mouse cDNA sequences
D. Schnerch, A., Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: nisc_mgc@nhgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,

Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,E.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLML at: http://lmage.llnl.gov Series: IRAL Plate: 5 Row: d Column: 14
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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CACTGGCACCATTGCCTCATTCAACATCAACACCCAACGCCTGGGTGGCCCGCTACATCTT CATGTACATGCTGATCTGGGGGAAGTTTGTGCTGTACAATATGTCACCTGTTGGCTGGT CATCACAGAAGACTATCTCCTCACTGAAGACTATGACAACCACCCCTTCTGGTTCCGCTG TCTCAAGCGCCTGAGTCTGGGCCTTTTCTACCTAGTGGGCTACACACTGCTCAGCCCCCA GCTGGTGCAGGGAGAGCTGATTGACATACCAGGAAAGATACCAAACAGCATCATTCCTGC CTCCTACTTCTATGGGGCCTTCTTGGTAGGGCCCCAGTTCTCAATGAATCACTACATGAA CTCCTACTATGGGGCCTTCTTGGTAGGGCCCCAGTTCTCAATGAATCACTACATGAA CTCTGAGCAACAGAAATATGCCATACGTGGTGTTCCCTTCCCTGCTGGAAGTTGCTGGTTT GAAGCTGATTGGCTGTTGACTACTTTGACGGAGGGAAAGATCAGAATTCCTTGTC GAAGCTGATTGGTTTGGCTGTTGACTACTTTGACGGAGGGAAAGATCAGAATTCCTTGTC TTACACTGCCACCGGCAACTACGATATCAAGTGGACAATGCCACATTGTGTTTCTGACTTT CTACCACTCCCTGCTGTATTGTGCTTCAGTTCCTCATCCTTCGACTAATGGGCCGCAC CTACCACTCCCTGCTGTGTATTGTGCTTCAGTTCCTCATCCTTCGACTAATGGGCCGCAC CCACCTCTTCCATACCTTTACAGGCCTCTCAATTGCTTATTTTAACTTTGGAAACCAGCT CCACCTCTTCCATACCTTTACAGGCCTCTCAATTGCTTATTTTAACTTTGGAAACCAGCT CACAGAAGGAGTATGCATTTTGACGGGCCTGGGCTTCAATGGCTTTGAAGAAAAGGGGCAA CACAGAAGGAGTATGCATTTTGACGGGCCTGGGCTTCAATGGCTTTGAAGAAAAGGGCAA CATGTACATGCTGATCTGGGGGCAAGTTTGTGCTGTACAAATATGTCACCTGTTGGCTGGT CATCACAGAAGACTATCTCCTCACTGAAGACTATGACAACCACCCCTTCTGGTTCCGCTG GCTGGTGCAGGGAGAGCTGATTGACATACCAGGAAAGATACCAAACAGCATCATTCCTGC 90.0%; ilarity 100.0%; Conservative ( Score 2045.4; ; Pred. No. 0; 0; Mismatches 0 1; 0 Gaps 1066 1006 466 187 406 127 346 67 847 787 946 667 886 607 826 547 766 487 706 427 646 367 586 307 526 247 727 0

759	928 CTACCACCCCCCCCATGGGGGGGGTGGAGAGGGGTGCAAGGCCCTGCCTG	σ.
	CTACCACCACCCCCCATGGGGGGGGGGGGGAGAGAGGGGGCCCTGCCTG	<
Db 361 ĠĊTĠĠTTTĊTĊ	2087 TCTAGCCAGGAATCTATTGTGTTTTTCTTCTGCCATTTTACTATGATTGTGTGTG	σ <
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241	1967 TGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAAGGGGAAACTCTTGTGGGAGG 2026	0 <
Qy 519 CTGACTTTGAA	1688 TGGCCAGGCTGGTCTCGAACTCCTGACCGCAAGTGATCCACCGCCTCCGCCTCCCAAAG 1747	0 4
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Db 121 GGCCGCACCAT	1847 GGCACGCCACCATGCCCAGCTAATTTTTGTATTTTCAGTAGAAACGGGATTTCACCACGT 1906	•
Db 61 AACCAGCTCTA Qy 399 GGCCGCACCAT	1/8/ CICCACCICCIGGGITCAAGICATTITCCTGCCTCAGCCTCCCAAGTAGCTGGGAATACA 1846	0 4
339	AGGCGTCTTGCTTTGTCACCCACGCTGGAATGCAGTGGCGGGATCTCAGCTCACCGCAAC 1	0
Db 1 TACCTCATCCA	1727 AGGCGTCTTGGCTTTGTCACCCACGCTGGAATGCAGTGGCGGGATCTCAGCTCACCGCAAC 1786	~
Matches 1842; Conserva  Qy 279 TACCTCATCCA	1448 GTGCCTCTGCCAGCCAAGTCTTCATTTGGGGCCAAAGGGGAAACTTTTTTTT	0 3
Query Match Best Local Similarity	CCTTTGCCCCAGAGCAGAGAAAAAAAGCCAGAGAGAGAAGATCGAAGCTTCCAGCT	. σ
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/org /mol /db	1547 TTCCCTGGTGGCCTGTGCGGGACTGGTGCAGAAACTACTCCGTCTCCCCTTTTCACAGGACT 1606	0 <
JOURNAL Fatent: WO 01 Avalon Pharma FEATURES SOURCE 1	1487 TTATATTCACAAAGCAATGGTGCCAAGGAAAGAAGATGTAAAGAAGATGGAATAATCCAT 1546 	σ <
AUTHORS Young, P.E., A Horrigan, S., TITLE Cancer gene deta	1427 GTATAAATCCATCTATTTCCTTGGCCACATCTTCTTCCTGAGCCTACTATTCATATTGCC 1486	σ <
ORGANISM Homo sapiens Eukaryota; Me Mammalia; Eut	1367 CTTCATGGGTTACTCCATGACTGCCTTCTGCCTCTTCACGTGGGACAAATGGCTTAAGGT 1426	<i>o &lt;</i>
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1988	1127 CAPACGACTCAAGTTCCTTGGAAATAAAGAACTCTCTCAGGGTCTCTCGTTGCTATTCCT 1186	0 <
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vative 0; Mismatches
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AGGGCCCCAGTTCTCAATGAATCAC 698	36	TGGTGTTCCTTCCCTGCTGGAAGTT 638	CTTTGACGGAGGGAAAGATCAGAAT 578 	N UI	CTTCCAGATGGCCTACCTTCTGGCT 458		CTCAATTGCTTATTTTAACTTTGGA 338 	6; Length 1842; 0; Indels 0; Gaps 0;		IGTATTTTCAGTAGAAACGGGATTT 1620 CGCAAGTGATCCACCCGCCTCCGCC 1958

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encoded by General Accession Number 2/5083; see corresponding genomic sequence in GenBank Accession Number 172506"  /codon_start=1 /product="C3f" /protein_id="AAC51640.1" /db_xref="G1:1673520" /translation="MGRTITAVLTTFCFQMAYLLAGYYYTATGNYDIKWTMPHCVLTL	a T \ \ L \ L	/dr /cr /ma	rect Submission  Molecular and Human Genetics, Baylbmitted (24-SEP-1996) Molecular and Human Genetics, Bayllege of Medicine, One Baylor Plaza, Houston, TX 77030, Location/Qualifiers  1. 1842  /organism="Homo sapiens" /mol_type="mRNA"	Large-scale sequencing in human chromosome 12p13: experiment computational gene structure determination genome Res. 7 (3), 268-280 (1997) 97228904 9074930 1 to 1842) Ansari-Lari M.A. Shen Y. Muzny D.M. Lee W. and Gibbs R A. Ansari-Lari M.A. Shen Y. Muzny D.M. Lee W. and Gibbs R A. Ansari-Lari M.A. Shen Y. Muzny D.M. Lee W. and Gibbs R A. Ansari-Lari M.A. Shen Y. Muzny D.M. Lee W. and Gibbs R A.	Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1842) Daarijari M & Chen V Marny D M Top W and Cibbs D A	HSU72515 1842 bp mRNA linear Human C3f mRNA, complete cds. U72515.	GTGGGAGGAGCAGAGGGGCTCACATCTCCCCTGATTCCCCCATGCACATTGCCTTATC TCTCCCCATCTAGCAGGAATCTATTGTGTTTTTTCTTCTGCC 2120	CACCACGTTGGCCAGGCTGGTCTCGAACTCCTGACCGCAAGTGATCCACCGCCTCCGCCTCCGCCTCCAAGTGATCCACCCGCCTCCGCCTCGCCAAGTGATCCAAAGTGATACAAAACTCTT	GGAATACAGGCACGCCACCATGCCCAGCTAATTTTTGTATTTTCAGTAGAAACGGGATTT

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oligo capping; fis (full insert sequence).

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I shibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S., Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S., Yamashita,H., Chiba,Y., Suzuki,Y., Hata,H., Kakagawa,K., Mizuno,S., Yamashita,H., Chiba,Y., Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S., Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and Sugano,S.

NEDO human cDNA sequencing project

Unpublished

E (bases 1 to 1573)

Sugano,S. and Suzuki,Y.

Direct Submission

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1474 TATTCATATTGCCTTATATTCACAAAGCAATGGTGCCAAGGAAAGAGAAGTTAAAGAAGA 1533	733 AATGGCTTAAGGTGTATAAATCCATCTATTTCCTTGGCCACATCTTCTTCCTGAGCCTAC 792	1414 AATGGCTTAAGGTGTATAAATCCATCTATTTCCTTGGCCACATCTTCTTCCTGAGCCTAC 1473	673 CCATCCACTGGCTCTTCATGGGTTACTCCACGACTGCCTTCTGCCTCTTCACGTGGGACA 732	1354 CCATCCACTGGCTCTTCATGGGTTACTCCATGACTGCCTTCTGCCTCTTCACGTGGGACA 1413	1294 CCCTGAGCAAGCTGGCCGCCATTACTGTCCTCCAGCCCTTCTACTATTTGGTGCAACAGA 1353	1239 IGGHAITICICATIGITATIGITGANAGHCAGGCIGCCAGGCICATICANAGHGCCCCA 1233	CGTTGCTATTCCTGGCCCTCTGGCACGGCCTGCACTCAGGATACCTGGTCTGCCTCCAGA	1174 CGTTGCTATTCCTGGCCCTCTGGCACGGCCTGCACTCAGGATACCTGGTCTGCTTCCAGA 1233	1114 CCCGCTACATCTTCAAACGACTCAAGTTCCTTGGAAATAAAGAACTCTCTCAGGGTCTCT 1173	1054 CAAACCCCGCTTCACTGGCACCATTGCCTCATTCAACACCAACGCCTGGGTGG 1113		994 AAGAAAAGGGCAAGGCAAAGTGGGATGCCTGTGCCAACATGAAGGTGTGGGCTCTTTGAAA 1053	253 CCTGTTGGCTGGTCACAGAAGGAGTATGCATTTTGACGGGCCTGGGCTTCAATGGCTTTG 312	CCTGTTGGCTGGTCACAGAAGGAGTATGCATTTTGACGGGCCTGGGCTTCAATGGCTTTG	874 TCTGGTTCCGCTGCATGTACATGCTGATCTGGGGCAAGTTTGTGCTGTACAAATATGTCA 933 	133 TGTTCATCAGCCAGCACTGAACAACCTTCGCGGGCACAGGGCTGTGCCAGAACCACCCCT 192	814 TGCTCAGCCCCCACATCACAGAAGACTATCTCCTCACTGAAGACTATGACAACCACCCC 87	/ Match 61.1%; Score 1388.2; DB 9; Length 1573; Local Similarity 97.7%; Pred. No. 0; Nes 1400; Conservative 0; Mismatches 33; Indels 0; Gaps 0;	/clone_Tib=TST" /clone_Tib=TST" /note="cloning vector: pME18SFL3" 158 a 436 c 378 g 401 t	/organism= rome septems /mol type="mrnn" /db_xref="caxon:9606" /clone="TST00701" /figume type="typefig"		Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for	(E-mail:conaleans: u-tokyo.ac.jp, 'El:81-3-5449-5286, Fax:81-3-5449-5416) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing:	Submitted (24-OCT-2001) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
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	AUTHORS	REFERENCE	ORGANISM	SOURCE	ACCESSION VERSION	AKO98090 LOCUS		. S	Db 1	ov pg	Q l	8 8			₽ 5	Q E	당 왕	B &	dg Vy	D Qy	Qγ	dg dg	g ç	Db
Otsuki, F., Sato, H., Ota, F., wakamatsu, A., 18111, S., 14114110, O., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K.,	Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Arita, M., Musashino, K., Yuki, H., Hara, T., Sugiyama	Mammalia; Eucheria; kodencia;	Mus musculus  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto	Mus musculus	C3f mRNA.  AK098090.1 GI:21758026  AK098090.1 Fiz (Fiz)	AK098090 2128 bp mRNA linear ROD 25-SEP-2002 N Mus musculus cDNA fis, clone TRACH2004292,highly similar to Human	1573 T 1573	ı—⊬		1453 TGTGTATGTGCCGCTACCACCACCCCCCCATGGGGGGTGGAGAGGGGTGCAAGGCCCT 1512 2194 GCCTGCTCCACTTTTTCTACCTTGGAACTGTATTAGATAAAATCACTTCTGTTTTGTTCAG 2253	TGTGTATGTGCCGCTACCACCACCCCCCCATGGGGGGGTGGAGAGGGGTGCAAGGCCCT	20/4 THATCTCTCCCCATCTAGCCAGGAATCTATTGTGTTTTTCTTCTGCCAATTTACTATGAT 1452		CTCTTGTGGGAGGAGCAGAGGGCTCACATCTCCCCTTGATTCCCCCCATGCACATTGCC	CCGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAAGGGGGAAA		1894 GATTTCACCACGTTGGCCAGGCTGGTCTCGAACTCCTGACCGCAAGTGATCCACCCGCCT 1953			1714 TITTTITGGAGAAGGCGTCTIGCTTIGTCACCCACGCIGGAAIGCAGIGGCGGGATCTC 1773 	1654 GATGCTTCCAGCTGTGCCTGCTGCCAGCCAAGTCTTCATTTGGGCCCAAAGGGGAAAC 1/13 	TTTTCACAGCACTCCTTTGCCCCAGAGCAGGAGATGGAAAAGCCAGGGAGGTGGAAGATC	153% IGGANIAM ICALITICCI INSUSPCE IN INCOMPARE	

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421 TCACTACCTTTTGCTTCCAGATGGCCTACCTTCTGGCTGG	301 CCTTTACAGGCCTCTCAATTGCTTATTTTAACTTTGGAAACCAGCTCTACCACTCCCTGC 360	120 AGATECGGGGGCTGTGGCCGAGGATCTGAGCCTTAACAAGTTGGCGACGTCTC 179  181 TGGGCGCGTCAGAACAGGCGCTGTGCGAGGATCTGAGCCTTTACCAGTTGGCGACGTCTC 240  181 TGGGCGCGTCAGAACAGGCGCTGCGGCTGATCATCTCCATCTTCCTGGGCTTACCCCTTTG 240  180 TGGGCGCGTCGGAACAGGCGCTGCCGCGCTCATCTTCTCCATCTTCCTGGGCTACCCGTTGG 239  241 CTTTGTTTTATCGGCATTACCTTTTCTACAAGGAGACCTACCT	61 GGGCTCCCGGAGTTAAGATGGCGTCCTCAGCGGAGGGGACGAGGGACTGTGGTGGCGC 1	ch 54.6%; Score 1240.4; DB 10; Length 2128; 1 Similarity 84.7%; Pred. No. 0; 433; Conservative 0; Mismatches 241; Indels 18; Gaps 3; 1 GGGGTGAAGCGATTTTGCCGGGATTCGGGGGGGGGGGGG	1. 2128 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="TRACH2004292" /note="cloning vector: pME18SFL3" 476 a 601 c 500 g 551 t	NEDO cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.  RAB; contain the sequencing of the seque	Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Sugiyama, A., and Isogai, T.  NEDO cDNA sequencing project Unpublished 2 (bases 1 to 2128) Isogai, T. and Yamamoto, J. Direct Submission Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
D Q D Q D 4	S B S B S	B & B & B	Q da Qy	o o o	D Q D Q	B Q B Q B	Q B Q B Q
CAATGGTGCCAAGAAAGGAAAAGTCACAGCACTCCCAGCTGTGCCTTG  CAATGGTGCCAAGAAAGAAAAGTTAAAAAAGAGGGAATGATCTCTGTCTTTCCCTGTG  GGCCTGTGCGGGACTGGTGCAGAAACTACTCGTCTCCCTTTTCACAGCACTCCTTTTGCCC  [	1381 CCATGACTGCCTTCTGCCTCTTCACGTGGACCAAATGCTTAAAGTGTATAAATCCATCT 1440  1380 CTATGACTGCCTTCTGCCTCTCTCACATGGACCAAATGCCTTAAAGTGTATAAATCCATCT 1439  1441 ATTTCCTTGGCCACATCTTCTTCCTGAGACCTAATTCATAATTGCCTTATAATTCAAAATGCAAAG 1500		1141 TCCTTGGAAATAAAGAACTCTCTCAGGGTCTCTCGTTGCTATTCCTGGCCCTCTGGCACG 1200	1021 CCTGTGCCAACATGAAGGTGTGGCTCTTTGAAACAACCCCCGCTTCACTGGCACCATTG 1080	901 TCTGGGGCAAGTTTGTGCTGTACAAATATGTCACCTGTTGGCTGGTCACAGAAGGAGTAT 960	720 AGCTGACTGACATACCAGGAAGATGCCAAACAGCACCATACCTGCTCTAAGCGCCCTGA 779  781 GTCTGGGCCTTTTCTACCTAGTGGGCTACACACTGCTCAGCCCCCACATCACAGAAGACT 840	1 AATATGCCATACGTGGTGTTCCTTCCCTGCTGGAAGTTGCTGGTTTCTCCTATTG

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TITLE
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                                                          source
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S. F., Zeeberg, B., Bucw, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R. F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T. E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
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Abramson, R. D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKerran, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
McKerran, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D. K., Muzny, D.M., Sodergren, E. J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R. W., Touchman, J.W., Green, E. D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
1278, 16899-16903 (2002)
1278, 16899-16903 (2002)
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                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at http://image.llnl.gov Series: IRAK Plate: 17 Row: h Column: 7 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/cdna/contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly
Kowis, C.R., Sneed, A.J., Martin, R.G., Muz
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Baylor College of Medicine Human Genom
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Submitted (27-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
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Eutheria; Rodentia;
/organism="Mus musculus"
/mol_type="mRNA"
                                                                            Location/Qualifiers
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     TCTGAGCAACAGAAATATGCCATACGTGGTGTTCCTTCCCTGCTGGAAGTTGCTGGTTTC
                                                                                                                    AAGCTGATTGGTTTGGCTGTTGACTTTTGACGGAGGGAAAGATCAGAATTCCTTGTCC
                                                                                                                                                                                                                                    TACACTGCCACCGGCAACTACGATATCAAGTGGACAATGCCACATTGTGTTCTGACTTTG
                                                                                                                                                                                                                                                                                         GTCACTGCCGTTATTACTACCCTTTGCTTCCAGATGGCCTACCTTCTTGCCGGATATTAC
                                                                                                                                                                                                                                                                                                                                   TACCACTCCTTGCTATGTGTCGTGCTTCAGTTCCTCATCCTGCGACTCATGGGCCGCACC
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VEKQVSSLIRDSPALSSLASITALQPFYYLVQQTIHWLFMGYSMTAFCLFTWDKWLKV
YRSIYFLGHVFFLSLLFILPYIHKAMVPRKEKLKKRE"
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IPGKMPNSTIPALKRLSLGLVYLVGYTLLSPHITDDYLLTEDYDNRPFWFRCMYMLIW
GKFVLYKYVTCWLVTEGVCILSGLGFNGFDENGTVRWDACANMKVWLFETTPRFNGTI
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/db_xref="LocusID:14792"
/db_xref="MGI:1315211"
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ductal carcinoma. 5 month old virgin mouse.
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/protein_id="AAH06753.2"
/db_xref="GI:14548370"
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/clone="MGC:11670 IMAGE:3709076"
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                                                                                                                 TCTTTCCCTGGTGGCCGAGAGCTGGACTGGTGCAGAAACTACTTGTCTCCCCTTCTCACAG
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;

1 (bases 1 to 1968)

Zhu,Y., Han,Y. and Reddy,J.K.

Cloning and initial characterization of mouse PTG cDN

expression is in a PPAR alpha dependent manner

Unpublished

(bases 1 to 1968)
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East Chicago Avenue, Chicago, IL 60611, USA
Location/Qualifiers
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                         TGGGCGCGTCAGAACAGGCGCTGCGGCTGATCATCTTCCATCTTCCTGGGTTACCCCTTTG
                                                                                                                                                                                            AGATGCGGGGGTGTGGGGGTGTCGAGGATCTGAGCCTTAACAAGTTGGCGACGTCTC
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/product="putative transmembrane protein PTG"
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/product="putative transmembrane protein PTG"
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VEKQVSSLIRDSPALSSLASITALQPFYYLVQQTIHWLFMGYSMTAFCLFTWDKWLKV
YRSIYFLGHVFFFLSLLFILPYIHXAMVPRKEKLKKRE"
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/strain="C57BL/6J"
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/chromosome="6"
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                                                                                                                                                                                                                                 Circle, Palo Alto, CA 94303, USA
This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sall and HindIII sites of the pDNN-DUNL vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.
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Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (Dases 1 to 1146)
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBa Phelan,M., and Farmer,A.
Cloning of human full-length CDSs in BD Creator(TM) S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCGAGAGCTGGACTGGCAGAAAACTACTTGTCTCCCTTCTCACAGCACTCCTCACCC
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                                         collection"
/lab_host="DH5alpha T1 resistant"
/note="Yector: pDNR-Dual"
                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GH00356X1.0"
/codon_start=1
/product="putative
                                                                                                                                                                                                organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:30582838
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                                                                                                                                                                             _type="mRNA"
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(Drosophila) mRNA,
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Best Local Similarity
Matches 1144; Conserv
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                                                                                                       CGCTACATCTTCAAACGACTCAAGTTCCTTGGAAATAAAGAACTCTCTCAGGGTCTCTCG
                                                                                                                                                AACCCCCGCTTCACTGGCACCATTGCCTCATTCAACATCAACACCAACGCCTGGGTGGCC
                                                                                                                                                                            AACCCCGCTTCACTGGCACCATTGCCTCATTCAACATCAACACCAACGCCTGGGTGGCC 1115
                                                                                                                                                                                                                          GAAAAGGGCAAAGTGGGATGCCTGTGCCAACATGAAGGTGTGGCCTCTTTGAAACA 1055
                                                                                                                                                                                                                                                                                       TGTTGGCTGGTCACAGAAGGAGTATGCATTTTGACGGGCCTGGGGCTTCAATGGCTTTGAA
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                                                                                    CGCTACATCTTCAAACGACTCAAGTTCCTTGGAAATAAAGAACTCTCTCAGGGTCTCTCG
                                                                                                                                                                                                           GAAAAGGGCAAGGCAAAGTGGGATGCCTGTGCCAACATGAAGGTGTGGCTCTTTGAAACA
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                          TTGCTATTCCTGGCCCTCTGGCACGGCCTGCACTCAGGATACCTGGTCTGCTTCCAGATG
                                                 TTGCTATTCCTGGCCCTCTGGCACGGCCTGCACTCAGGATACCTGGTCTGCTTCCAGATG 1235
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/db_xref="G1:30582839"
/db_xref="G1:30582839"
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WFRCMYMLIWGKEVLYKYYTCHLYTEGYCILTGLGFNGFEEKGKAKNDACANNKWHLF
ETNPRFTGTIASFNININAWVARYIFKRLKFLGNKELSQGLSLLFLALMHGLHSGYLV
CFQMKFLLYUIVERQAARLIQESFTLSKLAAITYLQFFYYLVQQTIHWLFMGYSMTAFC
LFTWDKWLKYKSIYFLGHIFFUSHLSLAGHTURGFKKKLKKME"

310 c 256 g 306 t
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99.9%;
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Pred. No. 1.7e-299;
0; Mismatches 1;
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GAATTCCTCATTGTTATTGTGGAAAGACAGGCTGCCAGGCTCATTCAAGAGAGCCCCACC 1295

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JOURNAL
REFERENCE
AUTHORS
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AUTHORS
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VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                               CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1356 ATCCACTGGCTCTTCATGGGTTACTCCATGACTGCCTTCTGCCTCTTCACGTGGGACAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      841 AAATTCCTCATTGTTATTGTGGAAAGACAGGCTGCCAGGCTCATTCAAGAGAGCCCCACC
                                                                                                                                                                                                                                                  Circle, Palo Alto, CA 94303, USA
This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloning system between the Sall and HindIII sites of the pDNR-DWAL vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bboinfo.clontech.com/orfclones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                artificial sequences.

1 (bases 1 to 1146)

Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Bisenstein,S.,
Kalnine,N., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
Cloning of human full-length CDSs in BD Creator(TM) System Donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (13-MAY-2003) BD Biosciences Clontech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 | [bases 1 to 1146]
Kalnine, N., Chen, X., Rolfe, A., Halleck, A., Hines, L., Eisenstein,
Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin,
Phelan, M. and Farmer, A.
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synthetic construct
synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vector
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/note="Vector: pDNR-Dual"
                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:32630"
/clone="GH00356L1.0"
                                        note="Mutations:
                                                                                                                                                                                                                   organism="synthetic construct"
                                                                                                                                        clone_lib="BD Creator(TM)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(CE 1 (bases 1 to 155975)

RS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Balbrooks, S.L., Benton, J., Binege, K., Blainkenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bulay, C., Burch, P., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Chavez, D., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Daris, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Daris, C., Davy-Carroll, L., Dederich, D.A., Duthwaite, K.J., Dragber, H., Dugan-Rocha, S., Durbin, K.J., Escotto, M., Falls, T., Ferragutto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogtes, M., Handlowsy, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Via, Y., Lia, J., Licharge, O., Liu, J., Lix, M., Loulseged, H., Lozado, R.J., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martindale, J., Martindale, A., Martinez, E., Massey, E., Mashiney, E., McLeod, M.P., Meador, M., Maicharde, P., Massey, E., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Voleco, R., Payton, B., Payton, B., Perz, L., Perze, L., Peters, M., Scherer, S., Scott, G., Shen, H., Shim, C., Shooshtari, N., Sisson, I., Sisson, I., Scherer, S., Scott, G., Shen, H., Shim, C., Shooshtari, N., Sisson, I., Sisson, I.,
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Birect Submission

Submitted (18-JUN-1999) Human Genome Sequencing of Molecular and Human Genetics, Baylor College of Molecular and Human Genetics, USA
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6 (bases 1 to 155975)
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4 (bases 1 to 155975)
CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
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Baylor Plaza, Houston, TX 77030, USA
On Apr 2, 2003 this sequence version replaced gi:4926863.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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Direct Submission

Submitted (04-APR-2003) Human Genome Sequencing Center, Departmented (04-APR-2003) Human Genome Sequencing Center, Departmented (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR-2003) Human Genome Sequencing (14-APR
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8 (bases 1 to 155975)
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Direct Submission
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ANNOTATION OF FEATURES:
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STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht

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260 0615	CT 2205	3CC 2145     3CC 60730	CC 2085	AG 2025     AG 60850	NAA 1965    NAA 60910	CACG 1905	AC 1845  - AC 61030	CGCAA 1785       CGCAA 61090	AG 1725    AG 61150	GC 1665	CAC 1605	ps 0;	
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Search completed: November 22, 2003, 05:56:24 Job time: 8298 secs

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Post-processing: Minimum Match 0%
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The present sequence encodes a human protein with hydrophobic domains. CC AAF75159 represents a shorter version of the present sequence. The CC protein possesses a hydrophobic domain and so is a secretory protein CC or a membrane protein. The protein is used as an antigen to prepare CC antibodies. The polynucleotide sequence is useful as a source of probes (for genetic diagnosis. It is also useful for producing the protein in large quantities and for gene therapy. The eukaryotic cells are used for detecting the receptors or ligands corresponding to the protein and CC for detecting small novel pharmaceuticals. The antibodies are also used for detection, quantification and purification of the proteins. Both the CC protein and polynucleotide may be used in research or as nutritional CC sources or supplements. The protein may have cytokine and cell CC sources or supplements. The protein may have cytokine and cell CC proliferation/differentiation activity, immune stimulating or suppressing CC activity, hemotopoiesis regulating activity, tissue growth activity, activity, hemostatic cand thrombolytic activity, receptor/ligand activity, anti-inflammatory CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory CC infectious diseases, cancer, sepsis, anaemias, burns and ulcers, CC immune deficiencies resulting from autoimmune disorders or complete response and enhance cognilation or inhibit to thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 120-124; 151pp; English.
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                                           mmune response and enhance coagulation or inhibit thrombosis
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Sequence 2264 BP; 482 A; 629 C; 550 G; 603 T; 0 other;

DB 22; Length

2264;

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AAZ50889 standard; CDNA;

(first

Human receptor-associated protein cDNA from Incyte clone

2906971

RAZSOBAT AAZSOBA XX AAZSZ XX AAZSZ XX AZSZ XX 31-M DT 31-M DT 31-M XX Huma XX Huma XX GYLC KW anti KW anti KW neuri Human receptor-associated protein; HRAP; Incyte clone 2906971; cytostatic; immunomodulatory; antiinflammatory; cardiant; antianaemic; antiarteriosclerotic; hepatotropic; antiarthritic antirheumatic; antiasthmatic; osteopathic; antiallergic; antidiabetic; dermatological; neuroprotective; diagnosis; treatment; prevention; reproductive disorder; cardiovascular; cell proliferative; autoimmune; inflammatory; allergy;

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                           This sequence is expressed in nervous, gastrointestinal and reproductive tissues. HRAP has cytostatic, immunomodulatory, antiinflammatory, cardiant, antiarteriosclerotic, hepatotropic, antiarthritic, antirheumatic, osteopathic, antiallergic, antianaemic, antiasthmatic, antidiabetic, dermatological and neuroprotective activities. The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with HRAP expression, especially cell proliferative, autoimmune/inflammatory, reproductive, cardiovascular and gastrointestinal disorders (e.g. atherosclerosis, cirrhosis, leukaemia, cancer, AIDS, arthritts, allergies, anaemia, asthma, dermatitis, diabetes, osteoporosis, multiple sclerosis and
                                                                                                                                                                                                                                                                                                         Sequence 2234 BP; 473 A; 626 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammatory,
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P-PSDB; AAY69987.
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                                                                                                    CAGTCGGGTTTCCAGGAGCTGAGCCTTAACAAGTTGGCGACGTCCCTGGGCGCCCCAGAA
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  CATTACCTTTCTACAAGGAGACCTACCTCATCCACCTCTTCCATACCTTTACAGGCCTC
                                                      CAGGCGCTGCGGCTGATCATCTCCCATCTTCCTGGGTTACCCCTTTGCTTTGTTTTATCGG
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Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
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Homo sapiens

WO200228999-A2

03-OCT-2001; 2001WO-US30821

03-OCT-2000; 2000US-237189P

LOGIC

Beazer-Barclay Y, Weissman SM, Yamaga ω Vockley

WPI; 2002-435328/46.

Detecting granulocyte activation by detecting differential export of genes associated with granulocyte activation, which serves diagnostic markers that is useful for monitoring disease state states and expression

Claim 1; SEQ ID No 991; 114pp; English

CC (GCA), by detecting the level of expression of gene(s) (GS) activation (CC (GCA), by detecting the level of expression of gene(s) (GS) identified by CC (DNA chip analysis as given in the specification, and comparing CC (CDNA chip analysis as given in the specification, and comparing CC (CDNA chip analysis as given in the specification and comparing CC (CDNA chip included are modulating (MS) GA by contacting GC with an agent CC (Also included are modulating (MS) GA by contacting GC with an agent CC (CDNA) in a tissue, an allergic response in a subject, exposure of a CC (CDNA) in a tissue, an allergic response in a subject, exposure of a CC (CDNA) in a tissue, an allergic response in a subject, exposure of a CC (CDNA) in a tissue, an allergic response in a subject, exposure of a CC (CDNA) in a tissue, an allergic response in a subject, exposure of a CC (CDNA) in a tissue, an allergic response in a subject, exposure of a CC (A) treating (MS) an inflammation (especially the CC (A) treating (MS) an inflammation (especially CDNA) in a tissue, an allergic response in a subject to a pathogen or sterile inflammatory disease, by detecting the CC (A) treating (MS) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen (CC (A) treating (MS) an inflammation (especially chronic) or in a tissue, an allergic response in a subject to a pathogen or sterile inflammatory disease, by contacting an agent capable of modulating (COA), MS is useful for screening an agent capable of modulating (COA), MS is useful for screening an agent capable of modulating (COA), MS is useful for screening an agent capable of modulating (COA), MS is useful for screening an agent capable of modulating (COA), MS is useful for screening an agent capable of modulating (COA), MS is useful for screening an agent capable of modulating (COA), MS is useful for screening an agent capable of modulating (COA), MS is useful for a pathogen or sterile (COA), MS is useful for screening the pathoge ftp.wipo:int/pub/published\_pct\_sequences

BP; 413 A; 525 C; 413 G; 491 T; 0 other;

Similarity 81.0%; 100.0%; Score 1842; Pred. No. 0 В Length 1842;

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WO200229103-A2. 11-APR-2002.	mecastatic liver tumour; cycostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.  Homo sapiens.	e; liver cancer; ds; hepatocellular carcinoma; hepatotropic;	ABN96918; 13-AUG-2002 (first entry)	SULT 5 N96918 ABN96918 standard; DNA; 1842 BP.	20/9 TCTCCCCATCTAGCCAGGAATCTATTGTGTTTTTCTTCTGCC 2120	019 GTGGGAGGAGGAGGGGCTCACATCTCCCCTCTGATTCCCC 019 GTGGGAGGAGCAGAGGGGCTCACATCTCCCCTTGATTCCCC 741 GTGGGAGGAGCAGAGGGGCTCACATCTCCCCTTGATTCCCC	59 TCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAAGGGGAAACTCTT	9 CACCACGTTGGCCAGGCTGGTCTCCAACTCCTGACCGCAGGTGATCCACCGCCTCCGCC	S GAATACAGGACGCCACCATGCCCAGCTAATTTTIGTATTTTCAGTAGAAACGGGATTT 61 GGAATACAGGCACGCCACCATGCCCAGCTAATTTTTGTATTTTCAGTAGAAACGGGATTT	779 ACCGGAACCTCCACCTCCTGGGTTCAAGTGATTTTTCCTGCTCAGCCTCCAAGTAGCTG 501 ACCGCAACCTCCACCTCCTGGGTTCAAGTGATTTTTCCTGCTCTAGCCTCCCAAGTAGCTG 501 ACCGCAACCTCCACCTCCTGGGTTCAAGTGATTTTTCCTGCCTCAGCCTCCCAAGTAGCTG 604 CTAATTAGGGAACGGAAGGGGAAGGGGAAGTGATTTTCCTGCTTCAGCTTCCCAAGTAGCTG		by TICCAGCIGIGCCICIGCCAGCCAAGICTICATITIGGGCCAAAGGGGAAACITITIT  11	S99 ACAGCACTICTTTTGCCCCAGAGCAGAGATGGAAAAGCCAGGGAGGTGGAAGATCGATGC	539 TAATICCATTICCCTGGTGGCCTGTGCGGGACTGGTGCAGAAACTACTCGTCTCCCTTTTC	7 AIAI GUCLIAIAI LUCAAAGCAA IGGIGCOAAGAAGAAGAAGA IAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA		359 CACTGGCTCTTCATGGGTTACTCCATGACTGCCTTCTGCCTCTTCACGTGGGACAAATGG	

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Best Local Similarity
Matches 1842; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a painvolves detecting the level of expression of two or more
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Best Local Similarity
Matches 1842; Conserv
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Soppet
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                       Claim
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P-PSDB; ABG06198.
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                              The present sequence encodes a human protein with hydrophobic domains. CC AAF25169 represents a longer version of the present sequence. The protein possesses a hydrophobic domain and so is a secretory protein CC or a membrane protein. The protein is used as an antigen to prepare CC antibodies. The polynuclectide sequence is useful as a source of probes CC for genetic diagnosis. It is also useful for producing the protein and CC in large quantities and for gene therapy. The eukaryotic cells are used CC for detecting small novel pharmaceuticals. The antibodies are also used CC for detection, quantification and purification of the protein and CC government of the protein and polynucleotide may be used in research or as nutritional CC governments. The protein may have cytokine and cell CC groliferation/differentiation activity, immune stimulating or suppressing CC activity, hematopoiesis regulating activity, tissue growth activity activity and tumour inhibition activity. It may therefore may be used to creat immune deficiencies resulting from autoimmune disorders or CC treat immune deficiencies resulting from autoimmune disorders or confectious diseases, cancer, sepsis, anaemias, burns and ulcers, commune response and enhance coagulation or inhibit thrombosis.
                                                                              Best Local Similarity Matches 1461; Conserv
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Best Local (
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                                                                                                                                          Sequence 1461 BP; 326 A; 401 C; 336 G; 398 T; 0 other;
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16-MAR-2000; 2000US-18962P.
25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
The invention relates to an isolated nucleic acid molecule (I) a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cance (b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate in a patient;
                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1137
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                                              TGCCAGCCAAGTCTTCATTTGGGGGCCAAAGGGGGAAACTTTTTTTGGAGAAGGCGTCTTGC
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                                                                                                                                                                                                                                                treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. carebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. AAS30580-AAS30685 represent novel human lung cancer antigen coding sequences. PCR primers and related sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at: ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel isolated lung cancer antigen polynucleotides (I) and polypeptides (II). (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) are also used in diagnosing a pathological condition or susceptibility to a pathological condition, in particular, lung cancer. The antibodies to (II) can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nouropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; autoimmune disease; rheumatoid arthritis; neoplasm; hyperproliferative disorder; cardiovascullar disorder; dardiovascullar disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hyperproliferative disorder; cardiovascular disorder; angiogenesis; nervous system disorder; Alzheimer's disease; infection; skin aging ocular disorder; wound healing; organ transplantation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; lung cancer; immunosuppressive; antiarthritic; antiproliferative; cytostatic; cardiant; vasotropic; nootropic; neuroprotective; antibacterial; virucide;
                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecule encoding a lung cancer antigen is in preventing, treating or ameliorating a medical condition
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The present invention relates to the isolation of novel human respiratory antigens (AAU17685-AAU17975), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing disorders related to the respiratory system including throat
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences.
                                                     ACA03402
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  22-MAY-2003
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Pred. No. 2.3e-187;
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DNA encoding human lung cancer antigen HIPAA05

KW Human; ds; gene; lung cancer antigen; anaemia; tissue regeneration;
KW constant region; immunotherapy; gene therapy; lung disorder; leukopenia;
KW small cell lung cancer; squamous cell carcinoma; adenocarcinoma; asthma;
KW respiratory disorder; nonallergic rhinitis; rheumatoid arthritis; ulcer;
KW adult respiratory distress syndrome; hyperprolliferative disorder; graft;
KW lung neoplasm; prostate neoplasm; immune system disorder; anaphylaxis;
KW ung neoplasm; blood-related disorder; allergic reaction; impotence;
KW inflammatory disorder; appendicitis; dermatitis; graft vs host disease;
KW immune complex disease; serum sickness; polyarteritis nodosa; arrhythmia;
KW urinary system disorder; glomerulonephritis; kidney failure; infertility;
KW cardiovascular disorder; myocardial infarction; osteoarthritis; aging;
KW musculoskeletal system disorder; Albers-Schonberg disease; cancer; burn;
KW meurological disorder; Alcheimer's disease; parkinson's disease; cancer; burn;
KW endocrine disorder; Addison's disease; diabetes mellitus; gastric reflux;
KW gastrointestinal disorder; reproductive system disorder; cerebral palsy;
KW developmental disorder; Farconi's syndrome; cellular level disease;
KW amyotrophic lateral sclerosis; infectious disease; viral infection;
XX
bacterial infection; wound healing.

Homo sapiens

US2002173454-A1

17-JAN-2001; 2001US-0764904 2000US-179065P

11-JUL-2000; 11-JUL-2000; 14-JUL-2000; 26-JUL-2000; 26-JUL-2000; 07-JUL-2000; 14-AUG 14-AUG-2000 14-AUG-2000 28-JUN-2000; 04-FEB-2000 31-JAN-2000; 2000US-225268P. 2000US-225270P. 2000US-225447P. 2000US-225757P. 2000US-224519P 2000US-225267P 2000US-180628P 2000US-214886P 2000US-224518P 2000US-220964P 2000US-218290P 2000US-217496P 2000US-216647P

2000US-228924P 2000US-226868P 2000US-225758P

2000US-229345P. 2000US-229509P. 2000US-229513P. 2000US-229287P. 2000US-229343P. 2000US-229344P.

2000US-231413P

2000US-234223P. 2000US-234274P. 2000US-234997P. 2000US-235834P

2000US-236327P. 2000US-236367P. 2000US-236368P. 2000US-236369P 2000US-236370P

14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 22-AUG-2000 30-AUG-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 05-SEP-2000 05-SEP-2000 05-SEP-2000 25-SEP-2000 21-SEP-2000 21-SEP 2000US-2000US-2000US-2000US-2000US-2000US-2000US-

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preventing and/
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08-DEC-2000;
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                                                                                   ATCTAGCCAGGAATCTATTGTGTTTTTTCTTCTGCCAATTTACTATGATTGTGTATGTGCC
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31-JAN-2000;
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16-MAR-2000;
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neurological disease;
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2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
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7-MAR-2000; 3-APR-2000; 3-MAY-2000;

2000US-0190076. 2000US-0198123. 2000US-0205515. 2000US-0209467.

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13-OCT 2000

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17-NOV he invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating
                                                                                      Nucleic acids encoding useful for preventing,
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                                            Disclosure; SEQ ID NO 7996; 1701pp + Sequence Listing; English
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                                                                            3224 human nervous system antigen polypeptides, diagnosing and/or treating nervous system -
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Pred. No. 5.1e-187;
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Human; nootropic; neuroprotective; cytostatic; dermatological; virucid immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerar antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine;
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CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating CC medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. CC The nucleic acids, proteins, antibodies and (antiagonists are useful CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC and ovarian cancer and other cancers of the adrenal gland, bone, bone CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and cepilepsy; and (f) infectious diseases such as viral, bacterial, fungal CC Note: The acommance data for the contraction of the contractions.
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Rosen CA, Barash SC, Ruben SM;

WPI; 2001-541565/60

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -

Disclosure; SEQ ID NO 12690; 1701pp + Sequence Listing; English

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune theroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (c) disease, and (f) infectious diseases such as viral, bacterial, fungal conditions.

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                                                                                                                                                                                                                                                            TGGTGCAGAAACTACTCGTCTCCCTTTTCACAGCACTCCTTTGCCCCAGAGCAGAATG
                                                                                                                                                                                                                                                                                                                 CAAGGAAAGAGAAGTTAAAGAAGATGGAATAATCCATTTCCCTGGTGGCCTGTGCGGVAC
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                                                                                                                  TTCATTTGGGGCCAAAGGGGAAACTTTTTTTTGGAGAAGGCGTCTTGCTTTGTCACCCAC
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/Cell type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/Cell line="JURKAT"
/Clone lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
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/db_xref="taxon:9606"
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7; Mismatches 47; I
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
                                                                                                                                                                                                                                                                                                           Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6809.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.ggi?seq=CSOD1040AB03QP1&cluster=6809.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
Feng Liang Email: fliang@lifetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Feb 15, 2001 this sequence version rep. Contact: Genoscope Genoscope - Centre National de Sequencage
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AL550083
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Faraday Avenue Genoscope sequence
Location/Qualifiers
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/tissue type="PLACENTA COT 25-NORMALIZED"
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/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVspORT 6 vector. Library was normalized
a 292 c 294 g 299 t 5 others
                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                               organism="Homo sapiens"
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AUTHORS	961 GCATTTTGACGGGCCTGGGCTTCAATGGCTTTGAAGAAAAGGGCAAAGTCGGATG 1020 	9 Q
JOURNAL I MEDLINE PUBMED	901 TCTGGGGCAAGTTTGTGCTGTKCAAATATGTCACCTGTTGGCTGGTCACAGAAGGAGTAT 960 	g 4g
	ATCTCCTCACTGAAGACTATGACAACCACCCCTTCTGGTTCCGCTGCATGTACATGCTGA	p B
<b>60 HJ</b>	1 ATCTCCTCACTGAAGACTATGACAACCACCCCTTCTGGTTCCGCTGCATGTACATGCTGA	Ş
	781 GTCTGGGCCTTTTCTACCTAGTGGGCTACACACTGCTCAGCCCCCACATCACAGAAGACT 840	B 8
	721 AGCTGATTGACATACCAGGAAAGATACCAAACAGCATCATTCCTGCTCTCAAGCGCCTGA 780 	Db Qy
	661 GGGCCTTCTTGGTAGGGCCCCAGTTCTCAATGAATCACTACATGAAGCTGGTGCAGGAG 720 	D Q
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REFERENCE AUTHORS	421 TCACTACCTTTTGCTTCCAGATGGCCTACCTTCTGGCTGG	Ş
JOURNAL MEDLINE PUBMED	361 TGTGTATTGTGCTTCAGTTCCTCATCCTTCGACTAATGGGCCGACCATCACTGCCGTCC 420	Qy Db
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JOURNAL I	241 CTTTGTTTTATCGGCATTACCTTTTCTACAAGGAGACCTACCT	γQ
REFERENCE AUTHORS	181 TGGGCGCGTCAGAACAGGCGCTGCGGCTGATCATCTCCATCTTCCTGGGTTACCCCTTTG 240	망왕
SOURCE I	198 TGGCGGGGTTCTGCAGTCGGGTTTCCAGGAGCTTAACAAGTTGGCGACGTCCC 257	DЬ
VERSION KEYWORDS	TGGCGGGGGTTCTGCAGTCGGGTTTCCAGGAGCTGAGCCTTAACAAGTTGGCGACGTCCC 1	ş
ACCESSION	61 GGGCTCCCGGAGTTAAGATGGCGTCCTCAGCGGAGGGGACGAGGGGACTGTGGTGGCGC 120	용 성
AK083687 LOCUS	79 GGGGGTGAAGCGATAGCTNTTGCCCGCATTCGGGGCGCGGAST-GGGGGGTCCCTGTG 137	Db
RESULT 3	GGGTGAAGCGATACGTTTTGCCCGCATTCGGGGCGCGCGC	Ş
Db 109	Best Local Similarity 98.4%; Pred. No. 3.2e-15; Matches 1038; Conservative 4; Mismatches 10; Indels 3; Gaps 3;	Best 1 Match
Qy 102	44.1%: Score 1002: DR 9:	Ouery

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RS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Razakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adashi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Salto, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Salto, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, I., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N.H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. P., Suzuki, H., and Hayashia, Y., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashia, Y., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashia, Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                             Nature 409
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                                                                                                                                                                                                                                                                    annotation of a full-length mouse cDNA collection (6821), 685-690 (2001)
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TITLE

Db 1 GTTATTĂCTĂCCCTTTGCTTCCĂĞĂTGGCCTĂCCTTGCTGCCĞĂŤĂTTĂCTĂCĂCĂGĞC 60  QY 477 ACCGGCAACTACGATATCAAGTGGACAATGCCACATTGTGTTCTGACTTTGAAGCTGATT 536	417 GTCCTCACTACCTTTTGCTTCCAGATGGCCTTACCTTCTGGCTGG	Query Match 41.9%; Score 952.4; DB 11; Length 1754; Best Local Similarity 85.4%; Pred. No. 2.9e-14; Matches 1090; Conservative 0; Mismatches 171; Indels 15; Gaps 2;	polyA_site 1754 /note="putative" BASE COUNT 437 a 477 c 383 g 457 t ORIGIN	al	DYYDGGKDGNSLTSEQQKYAIRGVPSLLEVAGFSYFYGAFLVGPQFSNNHYMKLVRGQ LTDLFGKMPNSTIPALKRLSLGLVYLVGYTLLSPHITDDYLLTGDYNNHYMKLPKTPRFN LIMGKFVLYKYVTCMLVTEGVCILSGLGFNGFDENGTVEMDACANMKVWLFETTPRFN GTIASRNINTMAWAYAFYIFKRENGFDENGLISLLFULAHGLHSGYTLGFOMEFL	/codon_start=1 /codeln_id="BAC38993.1" //bxcefln_id="BAC38993.1" //db_xref="GI:26350713" /translation="VITTLCFOMAXILLAGYYYTATGDYDIKWTMPHCVLTLKLIGLA	CDS <1. T1125 /note="unnamed protein product; putative unknown EST (GB BF302972, evidence: BLASTN, 98%, march=736)"	<pre>/clone="D030066012" /tissue type="whole body" /clone_Tib="RIKEN full-length enriched mouse cDNA library" /dev stage="9 days embryo"</pre>	/mol_type="mRNA" /strain="C57BL/6J" /db_xref="FAN70M_DB:D030066012" /db_xref="taxon:10090"		Please visit our web site for further details.  URL:http://genome.gsc.riken.go.jp/  URL:http://fantom.gsc.riken.go.jp/.	and Genome Science Laboratory in R	Fax:81-45-503-9216)  COMMENT CDNA library was prepared and sequenced in Mouse Genome  Encyclopedia Project of Genome Exploration Research Group in Riken	Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehizo-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-3922	itute	Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sal aki,D., Shibata,K., Shinagawa,A., Shiraki,T. agami,M., Tagawa,A., Takahashi,F., Takaku-Al anaka,T., Tomaru,A., Toya,T., Yasunishi,A.,	ani,K., Ishii,Y., Itoh,M., Kagawa,I., ai,J., Kojima,Y., Kondo,S., Konno,H., hara,C., Matsuyama,T., Miyazaki,A., M. Nishi,K., Nomura,K., Numazaki,R., Ohno	, 2 b.ū	of 60,770 full-length cDNAs JOURNAL Nature 420, 563-573 (2002)
1552 TGGTGGCCTGTGCGGGACTGGTGCAGAAACTACTCGTCTCCCTTTTTCACAGCACTCCTTT	Qy 1497 AAAGCAATGGTGCCAAGGAAAGAAGAAGATGAAGATGAATAATCCATTTCCC 1551	Qy 1437 Db 1021	TACTCCATGACTGCCTTCTGCCTCTTCAACGTGGGACAAATGGCTTAAGGTGTATAAATCC	Qy 1317 ACTGTCCTCCAGCCCTTCTACTATTTGGTGCAACAGACCATCCACTGGCTCTTCATGGGT	Qy 1257 GAAAGACAGGCTGCCAGGCTCATTCAAGAGAGCCCCACCCTGAGCAAGCTGGCCGCCATT 1316	Qy 1197 CACGGCCTGCACTCAGGATACCTGGTCTGCTTCCAGATGGAATTCCTCATTGTTATTGTG 1256	Qy 1137 AAGTTCCTTGGAAATAAAGAACTCTCTCAGGGTCTCTCGTTGCTAGTTCCTGGCCCTCTGG 1196	Oy 1077 ATTGCCTCATTCAACATCAACACCAACGCTTGGGTGGCCCGCTACATCTTCAAACGACTC 1136	Qy 1017 GATGCCTGTGCCAACATGAAGGTGTGGCTCTTTGAAACCAACACCCCGCTTCACTGGCACC 1076		Db 481 CTGATCTGGGGCAAATTTGTGCTGTACAAATACGTCACCTGCTGGTCACAGAAGGA 540	897 CTGATCTGGGGCAAGTTTGTGCTGTACAAATATGTCACCTGTTGGCTGGTCACAGAAGGA	Qy 837 GACTATCTCCTCACTGAAGACTATGACAACCCCCTTCTGGTTCCGCTGCATGTAACATG 896	OY 777 CTGAGTCTGGGCCTTTTCTACCTAGTGGGCTACACACTGCTCAGCCCCCACATCACAGAA 836	CY 717 GGAGAGCTGACTGACATACCAGGAAAGATACCAGAACAGCATCATTCCTGCTCTAAGCGC 776	OY 657 TATGGGGCCTTCTTGGTAGGGCCCCAGTTCTCAATGAATCACTACATGAAGCTGGTGCAG 716	OY 597 CAGAAATATGCCATACGTGGTGTTCCCTTCCTGGAAGTTGCTGGTTCTCCCTACTTC 656	Qy 537 GETTTGACTGTTGACCGAGGGAAAGATTCCTTGTCCTCTGAGCAA 596	

8 B 8	D Qy	B 8	Query Best Match	BASE COUNT ORIGIN			FEATURES sou				AUTHORS TITLE JOURNAL COMMENT	ORGANISM REFERENCE	ACCESSION VERSION KEYWORDS SOURCE	AL532090 LOCUS DEFINITION	Db RESULT	\$ \$	\$ <b>\$</b>
142 GTTTCCAGGAGCTGAGCCTTAACAAGTTGGCGACGTCCTGGGGGGGCGGTCAGAACAGGGGG 201	82 CGTCCTCAGCGGAGGGGGACGAGGGGACTGTGGTGGCGGTGGCGGGGGTTCTGCAGTCGG 141	22 GCCGCATTCGGGGCGCGGACTGGGGGGGTCCCTGTGGGGCTCCCGGAGTTAAGATGG 81	Query Match 40.9%; Score 930.4; DB 9; Length 1000; Best Local Similarity 98.5%; Pred. No. 1.4e-13; Matches 938; Conservative 1; Mismatches 13; Indels 0; Gaps 0;	210 8	/clone lib="Homo sapiens FETAL LIVER" 6; 1st strand cDNA /note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and clone was digest	<pre>/db_xref="taxon:9606" /clone="CSODMO4YH02" /tissue_type="FETAL LIVER" /dev_stage="fetal"</pre>	rce	<pre>cgi-bin/cluster.cgi?seq=CSODM004DD01QP1&amp;cluster=6809.f. Contact :     Feng Liang Email : filang@lifetech.com URL :     http://fulllength.invitrogen.com/ InVitroGen Corporation 1600     Faraday Avenue Genoscope sequence ID : CSODM004DD01QP1.</pre>	Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6809.f For more information about this cluster, see http://www.genoscope.cns.fr/	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: Begrefædenoscope ons fr. Web : www.genoscope ons fr	AL RS	4 Homo sapiens Eukaryota; Me Mammalia; Eut 1 (bases 1 t		ğ	1251 TCTGCGACAGCCAAAG 1266 4	1672 TCTGCTGCCAGCCAAG 1687	GCCCCAGAGCAGAATGGAAAAGCCAGGGAGGTGGAAGATCGATGCTTCCAGCTGTGCC
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COMMENT	REFERENCE AUTHORS TITLE JOURNAL	SOURCE ORGANISM	ACCESSION VERSION	RESULT 5 BX339313 LOCUS	Db .	Db Qy	B 8	ος Ογ	D Qy	B Qy	Qy Db	Db ?	B &	Db Qy	Д Qy	B &	
Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 9106 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of		ens (human) ens ens (Chordata, Craniata, Vertebrata, E	BX339313 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens clone CSODIO70YJ16 5-PRIME, mRNA sequence. BX339313 BX339313.1 GI:30335787	mRNA linear ES	922 ACAAATATGTCACCTGTTGGCTGGTCACAGAAGGAGTATGCATTTTGACGGG 973 	862 ACAACCACCCCTTCTGGTTCCGCTGCATGTACATGCTGATCTGGGGCAAGTTTGTGCTGT	802 TGGGCTACACACTGCTCAGCCCCCACATCACAGAAGACTATCTCCTCACTGAAGACTATG	742 AGATACCAAACAGCATCATTCCTGCTCTCAAGCGCCTGAGTCTGGGCCTTTTCTACCTAG	682 AGTTCTCAATGAATCACTACATGAAGCTGGTGCAGGGAGAGCTGATTGACATACCAGGAA 	622 CTICCCTGCTGGAAGTTGCTGGTTTCTCCTACTTCTATGGGGCCTTCTTGGTAGGGCCCC	562 GAGGGAAAGATCAGAATTCCTTGTCCTCTGAGCAACAGAAATATGCCATACGTGGTGTTC	502 CAATGCCACATTGTGTTCTGACTTTGAAGCTGATTGGTTTGGCTGTTGACTACTTTGACG	442 TGGCCTACCTTCTGGCTGGATACTATTACACTGCCACCGGCAACTACGATATCAAGTGGA 	382 TCATCCTTCGACTAATGGGCCGCACCATCACTGCCGTCCTCACTACCTTTTGCTTCCAGA	322 CTTATTTTAACTTTGGAAACCAGCTCTACCACTCCCTGCTGTGTATTGTGCTTCAGTTCC	262 THITCHACAAGGAGACCTACCTCATCCACTCTTCCATACCTTTACACGCCTCTCAATTG	9

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http://www.genoscope.cns.fr/
gj.-bin/cluster.cg1/seq-CSODIO70DE08QP1&cluster=6809.f. Contact:
feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO70DE08QP1.
Location/Qualifiers
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/tissue type="PLACENTA COT 25-NORMALIZED"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
a 285 c 285 g 298 t 41 others
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/mol_type="mRNA"
/db_xref="taxon:9606"
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5; Mismatches
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1092 ATCAACACCAACGCCTGGGTGGCCCGCTACATCTTCAAACGACTCAAGTTCCTTGGAAAT 1151
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                                                      962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: LLCM1967 row: e column: 20

High quality sequence stop: 677.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1053)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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BM557200
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AGENCOURT_6579051 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5466619
                                                      Similarity 95.
62; Conservative
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                                                                                                                                                        230
                                                                                                                                                /tissue_type="amelanotic melanoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_41"
/clone="Forgan: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
/note="Forgan: skin; Vector: pOTB7; Site 1: XhoI; Cloned into EcoRI/KhoI sites using the following 5: adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

30 a 313 c 237 g 267 t 6 others
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                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:5466619"
                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                         39.9%;
95.4%;
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                                                      Score 906.4;
Pred. No. 4.4e
0; Mismatches
                                                                         906.4; DB 1
No. 4.4e-13;
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AL532089 Homo sapiens FETAL LIVER Homo sapiens cDNA clone CS0DM004YH02 3-PRIME, mRNA sequence.
AL532089 AL532089 AL532089 GI:31069921 EST.
                                                                                                                               CCTCTGATTCCCCCATGCACATTGCCTTATCTCTCCCCATCTAGCCAG
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Query Match
Best Local Similarity
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Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 958)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6809.f
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DM004DD01NP1&cluster=6809.f. Conta
Feng Liang Email: fliang@nifetech.com URL:
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DM004DD01NP1.
Location/Qualifiers
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On Feb 13, 2001 this sequence version replaced
Contact: Genoscope
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BP 191 91006 EVRY cedex - France
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CTGTGCCTCTGCTGCCAGCCAAGTCTTCATTTGGGGCCAAAGGGGAAAC-TTTTTTTTGG
                                                                                                            CTCCTTTGCCCCAGAGCAGAGAATGGAAAAGCCAGGGAGGTGGAAGATCGATGCTTCCAG
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/clone_lib="Homo sapiens FETAL LIVER"
/clone_lib="Homo sapiens FETAL LIVER"
/clone_stage="fetal"
/clone_stage="fetal"
/clone_stage="fetal"
/clone_stage="fetal"
/note="Organ; liver; Vector: pCMVSPORT 6; lst strand cDNA
/note="Organ; liver; Vector: pCMVSPORT 6; lst strand cDNA
/note="Organ; liver; Vector: pCMVSPORT 6]
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."
229 c 272 g 210 t 7 others
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/db_xref="taxon:9606"
/clone="CSODM004YH02"
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Pred. No. 4.8e-13;
4; Mismatches 11
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FEATURES Source	RESULT B AL557774 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
	AL557774 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED Homo sapiens cDNA clone CSODJ003YA18 5-PRIME, mRNA sequence.  AL557774 AL557774.2 GI:31279574  EST. Homo sapiens (human)  M Homo sapiens (human)  M Homo sapiens (human)  M Homo sapiens (Example Contact; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 1201)  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  Full-length cDNA libraries and normalization  Unpublished  On Feb 15, 2001 this sequence version replaced gi:12901710.	1724 AGAAGGCGTCTTGCTTTGTCACCCACGCTGGAATGCAGTGGCGGGATCTCAGCTCACCGC 1783 480 AGAAGGCGTCTTGCTTTGTCACCCACGCTGGAATGCAGTGGCGGGATCTCAGCTCACCGC 421 1784 AACCTCCACCTCCTGGGTTCAAGTGAATTTTCCTGCCTCAGCCTCCCAAGTAGCTGAGAT 1843 420 AACCTCCACCTCCTGGGTTCAAGTGATTTTCCTGCCTCAGCCTCCCAAGTAGCTGGGAAT 1843 420 AACCTCCACCTCTGGGTTCAAGTGATTTTCCTGCCTCAGCCTCCCAAGTAGCTGGGAAT 361 1844 ACAGGCACGCCACCATGCCCAGCTAATTTTTGTATTTTCAGTAGAAACGGGATTTCACCA 1903 1844 ACAGGCACGCCACCATGCCCAGCTAATTTTTGTATTTTCAGTAGAAACGGGATTTCACCA 1903 1894 ACAGGCACGCCACCATGCCCAGCTAATTTTTGTATTTCAGTAGAAACGGGATTTCGCCA 1963 1894 ACAGGCACGCCTGGGTCTCGAACCTCCTGACCGCAAGTGATCCACCCGCCTCCCCA 241 1904 CGTTGGCCAGGCTGGTCTCGAACCTCTGACCGCAAGTGATCCACCCGCCTCCCCA 241 1904 AGGTGCTGGGATTACAGCGGTAAGCCCACCCGGCCCAAAGGGGAAACTCTTTGTGGG 2023 1904 AAGTGCTGGGATTACAGCGGTAGAGCCACCCGGCCCCAAAGGGGAAACTCTTTGTGGG 2023 1914 AAGTGCTGGGATTACAGCGTGAGCCACCCGTGCCCCGGCCCCAAAGGGGAAACTCTTTGTGGG 2023 1904 AAGTGCTGGGATTACAGCGTGAGCCACCCGTGCCCCAAAGGGGAAACTCTTTGTGGG 181 2024 AGGAGCAGAGGGGCTCACATCTCCCCCTCTGATTCCCCCCATGCAAAGGGAAACTCTTTTCTTCTCC 2083 110 AGGAGCAGAGGGGCTCACATCTCCCCCTCTGATTCCCCCCATGCACACATTGCCTTATTCTCTCC 2083 110 AGGAGCAGAGGGGCTCACATCTATTTTTTTTTTTTTCTCTCTC
2 2 2 5 5 5 5 5 5 5 6 6 6 6 6 6 6 6 6 6	8	BASE COUNT ORIGIN Query Ma Query Ma Best Loc Matches  Qy  Db  Qy  Db  Qy  Db  Qy  Db  Qy  Db  Qy  Db  Qy  Db
GCTGGAAGTTGCTGGTTTCTCCTACTTCTATGGGGCCTTCTTGGTAGGGCCCAGTTCTCCAATGGGGCCTTCTTGGTAGGGCCCCAGTTCTCCAATGGGGCCTCACTTCTTGGTAGGGCCCCAGTTCTCCAAGTACCAGAAAGATACCAAGAATACCAGAAAGATACCAGAAAGATACCAGAATCACTACATGAAGCTGGTGCAGGGAAGAGATACCAAAGATACCAAGAATCACTACATACA	313 TAACTTTGGAACCAGCTCTTACCACTCCTGCTGTTGTTTTGCTTCCAGATTGCCCTACCTA	/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR v sites of the pcwVspORT 6 vector. Library was normalized."  38.4%; Score 873.4; DB 9; Length 1201; Local Similarity 91.0%; Pred. No. 2.2e-12; hes 956; Conservative 32; Mismatches 50; Indels 12; Gaps 6;  29 TTCGGGGCGCGGACTGGGGGGTCCCTGTGGGGGTTCCCGGAGTTAAGATGGCGTCCTC 72  89 ACCGGAATCCCGGACTGGGGGGACTGTGGCGCTCCCGGAGTTAAGATGGCGTTCCA 148

Qy 1360 ACTGGCTCTTCATGGGTTACTCCATGACTGCCTTCTTCCCTTCTGCGACAAATGGC 1419	Qy 1300 GCAAGCTGGCCGCCATTACTGTCCTCCAGCCCTTCTACTATTTGGTGCAACAGACCATCC 1359      :	Qy         1240         TCCTCATTGTTATTGTGGAAAGACAGGCTGCCAGGCTCATTCAAGAGAGAG	Query Match  38.0%; Score 864.8; DB 9; Length 1065;  Best Local Similarity 91.8%; Pred. No. 3.7e-12;  Matches 896; Conservative 28; Mismatches 49; Indels 3; Gaps 3;	digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."  BASE COUNT 259 a 205 c 302 g 228 t 71 others	<pre>/tissue_type="PLACENTA COT 25-NORMALIZED" /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="lst strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was</pre>	/or /mo /db /cl	http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 FEATURES FARTURES Location/Qualifiers SOURCE 11065		BP 191 91006 EVRY cedex - France BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This semience belongs to semience cluster sand from	AL.	Primates; Catarrhin; Hominidae; Jessee, J. and Polayes, D. Staries and normalization	S EST.  Homo sapiens (human) ISM Homo sapiens Eukaryota: Metazoa: Chordata:	<pre>clone CS0DI040YC05 3-PRIME, mRNA sequence. N AL574064.2 GI:31295399</pre>	AL574064 AL574064 1065 bp mRNA linear EST 31-MAY-2003 DEFINITION AL574064 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA	RESULT 9	Qy 1049 TGAAACAACCCCCGCTTCACTGGCACCAT 1078	QY 989 CTTYGAAGAAAAGGGCAAAGTGGGATGCCTGTGCCAACATGAAGGTGTGCTCTT 1048	908 TATGKCACYGTTGGYKGKCMCAGAAGGA-KATGSMTTTTGACGGGCSGGGYTCAATGG
and Polayes,D. I normalization version replaced gi:12	SOURCE Homo sapiens (human) SOURCE Homo sapiens ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia, Eutheria, Drimates, Caparrhini, Hominidae, Homo	z Ç	AL579737 Homo camions T CELLS (HIDEAT CELL LINE)	QY 2200 TCCACTTTTCTACCT 2215	OY 2140 TGTGCCGCTACCACCCCCCCCATGGGGGGTGGAGAGGGGTGCAAGGCCCTGCCTG	Qy 2080 CTCCCCATCTAGCCAGGAATCTATTGTGTTTTTCTTCTGCCAATTTACTATGATTGTGTA 2139     :  :   :    :	Qy 2020 TGGGAGGAGCAGAGGGGCTCACATCTCCCCTCTGATTCCCCCCATGCACATTGCCTTATCT 2079	Qy 1960 CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGAAAGGGGAAACTCTTG 2019	OY 1900 ACCACGTTGGCCAGGCTGGTCTCGAACTCCTGACCGCAAGTGATCCACCCGCCTCCGCCT 1959	Qy 1840 GAATACAGGCACGCCACCATGCCCAGCTAATTTTTGTATTTTCAGTAGAAACGGGATTTC 1899	Oy 1780 CCGCAACCTCCACCTCCTGGGTTCAAGTGATTTTCCTGCCTCAGCCTCCCAAGTAGCTGG 1839	Qy 1720 TTGGAGAAGGCGTCTTGCTTTGTCACCCACGCTGGAATGCAGTGGCGGGATCTCAGCTCA 1779	554 TCCAGCTGTGCTCTGCTYCCAGCCAAGTCTTCATTTGGGGCCAAAGSGSAAACTTTTTT	OY 1660 TCCAGCTGTGCCCTGCTGCCAGCCAAGTCTTCATTTGGGGGCAAAGGGGAAACTTTTTT 1719	1600 CAGCACTCCTTTGCCCCCAGAGCAGAGAATGGAAAAGGCCAGGGAGGTGGAAGATCGATGCT 1	Qy 1540 AATCCATTTCCCTGGTGGCCTGTGCGGGACTGGTGCAGAAACTACTCGTCTCCCTTTTCA 1599	QY 1480 TATTGCCTTATATTCACAAAGCAATGGTGCCAAGGAAAGAAGATTAAAGAAGATGGAAT 1539	794 TTAAGGTGTATAAATCCATCTATTTCYTTGGCCACATCTTCTTCCTGAGCCTACTATTCA

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FEATURES
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1815 CTGCCTCAGCCTCCCAAGTAGCTGGGAATACAGGCACGCCACCCATGCCCAGCTAATTTTT
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6809.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODJ003BA09NP1. Location/Qualifiers
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                                                              AATGCAGTGGCGGGATCTCAGCTCACCGCAACCTCCACCTCCTGGGTTCAAGTGATTTTC
                                                                                                                                                           TTGGGGCCAAAGGGGAAACTTTTTTTTGGAGAAGGCGTCTTGCTTTGTCACCCACGCTGG
                                                                                                                                                                                                                                                         CAGAAACTACTCGTCTCCCTTTTCACAGCACTCCTTTGCCCCCAGAGCAGAAATGGAAAA
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                                          AATGCAGTGGCGGGATMAMAGCTMACCGCAACCTCCACCTCCTGGGTTCAAGTGATTTTC
                                                                                                                                  TTGGGGCCAAAGGGGAAACTWWTTATTGGAGAAGRCATCTTGCTTTGTMACCCACGCTGG
                                                                                                                                                                                                                   GCCAGGGAGGTGGAAGATCGATGCTTCCAGCTGNGCCNCNGCNGCCAGCCAAGNCNNCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCTTCTTCCTGAGCCTACTATTCATATTGCCTTATATTCACAAAGCAATGGTGCCAAGG
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247 c 334 g 250 t 112 others
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/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
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/db_xref="taxon:9606"
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10-NORMALIZED"
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Pred. No. 5.2e-12;
0; Mismatches 42
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cgi-bin/cluster.cgi?seq=CSDDI072AH10NP1&cluster=6809.f. (
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation
Faraday Avenue Genoscope sequence ID : CSODI072AH10NP1.
                                                                                                                                                                                                                                                                                                                                                                                                                          BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6809 more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
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                /tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oilgo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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/mol_type="mRNA"
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1 (bases 1 to 1097)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: DCTD/DTP
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://inage.lnl.gov

Plate: LLCM1968 row: h column: 07
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                                  CACATCTTCCTGAGCCTACTATTCATATTGCCTTATATTCACAAAGCAATGGTGCCA
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     CACATCTTCTTCCTGAGCCTACTATTCATATTGCCTTATATTCACAAAGCAATGGTGCCA
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_41"
/clone_lib="NIH MGC_41"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                         Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6809.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi7seg=CSOBAG065ZE03_CS06165_1&cluster=6809.f.
Contact: Feng Liang Email: fliang@lIfetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faradday Avenue Genoscope sequence ID: CSOBAG065ZE03_CS06165_1.
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 876)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
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BX431852 BX431852.1 GI:30779040
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                                                                                                                                        AATGGTGCCAAGGAAAGAGAAGTTAAAGAAGATGGAATAATCCATTTCCCTGGTGGCCTG
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/note="Organ: liver; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."
a 237 c 201 g 227 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="CS0DM004YH02"
/tissue_type="FETAL LIVER"
/dev_stage="fetal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 1.7e-11;
0; Mismatches 7;
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1680

1621

722

782

1561 662 1501 602 1441

542 1381 482 1321

1261

422

1201

362

1141

302

392

572

480 512 420 452 360

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REFERENCE
AUTHORS
TITLE
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Best Local S
Matches 883
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AGENCOURT 8801447 NIH_MGC_129 M
5', mRNA sequence.
BQ917856
BQ917856.1 GI:22332554
EST.
Mus musculus (house mouse)
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                              241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
cDNA Library Preparation: Rescen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC more distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://image.llnl.gov
Plate: LLAM13734 row: n column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National
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                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                            GAGACCTACCTCCACCTCTTCCATACCTTTTACAGGCCTCTCAATTGCTTATTTTAAC
                                                                                                            ATCTCCATCTTCCTGGGTTACCCCTTTGCTTTGTTTTATCGGCATTACCTTTTCTACAAG
                                                                                                                                                              CTGAGCCTTAACAAGTTGGCGACGTCCCTGGGCGCGCTCAGAACAGGCGCTGCGGCTGATC
                                                                                                                                                                                               CTGAGCCTTAACAAGTTGGCGACGTCCCTGGGCGCGCTCAGAACAGGCGCTGCGGCTGATC
                                                                                                                                                                                                                              GAGGGGACGAGGGACTGTGGTGGCGCGCTGGCGGGTTTCTGCAGTCGGGTTTTCCAGGAG
                                                                                                                                                                                                                                                               GAGGGGGACGAGGGACTGTGGTGGCGCTGGCGGGGTTCTGCAGTCGGGTTTCCAGGAG
                                                                                                                                                                                                                                                                                               GGTAGCGAGGCCTGGGTGGCGAATTCGGCACGAGGCGGAGTTAAGATGGCGTCCTCAGCG
                                                                                                                                                                                                                                                                                                                      GGGCGCGGACTGGGGGGTCCCTGTGGGGCTCCCCGGAGTTAAGATGGCGTCCTCAGCG
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                            GAGACCTACCTCATCCACCTCTTCCATACCTTTACAGGCCTCTCAATTGCTTATTTTAAC
                                                                                            ATCTCCATCTTCCTGGGTTACCCCTTTGCTTTGTTTTATCGGCATTACCTTTTCTACAAG
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      /moi_type="mRNA"
/db xref="taxon:10090"
/clone="IMAGE:6311255"
/clone="IMAGE:6311255"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_129"
/note="Corgan: olfactory epithelium; Vector:
/note="Corgan: olfactory epithelium; Vector:
/note="Corgan: olfactory site_1: EcoRV; Site_2: Noti; Cloned unidirectionally. Primer: Oligo dT. Average insert size
2:2 kb. Constructed by ResGen, Invitrogen Corp. Note: this
is a NIH_MGC_Library."
99 a 260 c 248 g 267 t
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l Institutes of Health, Mammalian Gene
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                      Score 836.4; DB 13; Pred. No. 1.7e-11;
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          FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Pocus
                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                 AUTHORS
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11527 row: m column: 21
High quality sequence stop: 840.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
BI767794
BI767794.1 GI:
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; V
Mammalla; Eutheria; Primates; Catarrhini;
1 (bases 1 to 882)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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603060787F1_NIH_MGC_122
                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                     GI:15759372
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	CAG 1577	GAGAAGTTAAAGAAGATGGAATAATCCATTTCCCTGGTGGCCTGTGCGGGACTGGTG	1518	Ş
•	  AA 720	TTCTTCCTGAGCCTACTATTCATATTGCCTTATATTCACAAAGCAATGGTGCCAAGGAAA	. 661	뫄
	AA 1517	TTCTTCCTGAGCCTACTATTCATATTGCCTTATATTCACAAAGCAATGGT	1458	ð
	TC 660	TCTTCACGTGGGACAAATGGCTTAAGGTGTATAAATCCATCTATTTCCTCTGGCCACATC	601	멍
	VTC 1457		1399	ð
	900 	ATTTGGTGCAACAGACCATCCACTGGCTCTTCATGGGTTACTCCATGACTGCCTTCTGCC	541	밁
	CC 1398		1339	ð
	CT 540 .	TTCAAGAGAGCCCCACCCTGAGCAAGCTGGCCGCCATTACTGTCCTCCAGCCCTTCTACT	481	밁
	CT 1338		1279	Ş
	CA 1278	TGGTCTGCTTCCAGATGGAATTCCTCATTGTTATTGTGGAAAGACAGGCTGCCAGGCTCA	1219 421	유
	CC 420	TCTCTCAGGGTCTCTCGTTGCTATTCCTGGCCCTCTGGCACGGCCTGCACTCAGGATACC	361	В
	CC 1218		1159	ş
	AC 360	CCAACGCCTGGGTGGCCCGCTACATCTTCAAACGACTCAAGTTCCTTGGAAATAAAGAAC	301	망
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	σ	TAGTGGGCTACACACTGCTCAGCCCCCACATCACAGAAGACTATCTCCTCACTGAAGACT	<b>1</b>	망
	CT 858		799	ð
	)s 3;	Similarity 99.0%; Pred. No. 2.7e-11; S; Conservative 0; Mismatches 6; Indels 3; Gap	Query Match Best Local Simil Matches 865; (	
	SPORT6; ile igo-dT royed royed royed royed royed royed royed royed	/organism="Homo sapiens" /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5210300" /lab host="MIH_MGC 122" /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH MGC Library."	SOURCE	BA ORA

Search completed: November 22, 2003, 03:38:01 Job time: 4752 secs

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cgi-bin/cluster.cgi?seq=CSODIO40ABO3QP1&cluster=6809.f. Contact Feng Liang Email : fliang@lifetech.com URL :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1 AL550083 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT		C 6 7 6 6 7 6 7 6 7 6 7 7 7 7 7 7 7 7 7
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/note="Jst strand cDNA was primed with a NotI-oligo(dT)
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153 CTGAGCCTTAACAAGTTGGCGACGTCCCTGGGCGCTCAGAACAGGCGCTGCGGCTGATC 212	93 GAGGGGACGAGGGGACTGTGGTGGCGCTGGCGGGGGTTTCGCAGTCGGGTTTCCAGGAG 152	Match 38.8%; Score 881; DB 9; Length 1000; Local Similarity 100.0%; Pred. No. 7.5e-142; es 881; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AL532090 Homo sapiens FETAL LIVER Homo sapiens cDNA clone CSODMO14YHO2 5-PRIME, mRNA sequence. AL532090 AL532090 AL532090 AL532090 AL532090 AL532090 AL532090 AL532090 AL532090 AL532090 AL532090 AL532090 Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human)  Li, Wasca I to 1000) Li, Wasca I to 1000 Li, Wasca I to 1000 Li, Wasca I to 1000 Li, Wasca I to 1000 Li, Wasca I to 1000 Reb 13, 2001 this sequence version replaced gi:12795583. Contact: Genoscope Genoscope. Centre National de Sequencage Brisl 91006 EVRY cedex - France Brisl 91006 EVRY cedex - Fr	1007 G 1007   1084 G 1084	947 CACAGAAGGAGTATGCATTTTGACGGGCCTGGGCTTCAATGGCTTTGAAGAAAAGGGCAA 1006 	827 CATCACAGAAGACTATCTCCTCACTGAAGACTATGACAACCACCCCTTCTGGTTCCGCTG 886

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  Unpublished
Contact: Genoscope
Genoscope - Centre
                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                           BX431852
BX431852 Homo sapiens FETAL LIVER Homo sapiens CS0DMO04YHO2 5-PRIME, mRNA sequence.
BX431852
BX431852
BX431852.1 GI:30779040
                                      Li,W.B., Gruber,C., Jessee
Full-length cDNA libraries
                                                                                                        Homo sapiens (human)
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Best Local Similarity
Matches 784; Conserv
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CTTCTTCCTGAGCCTACTATTCATATTGCCTTATATTCACAAAGCAATGGTGCCAAGGAA
                                               CCTCTTCACGTGGGACAAATGGCTTAAGGTGTATAAATCCATCTATTTTCCTTGGCCACAT
                                                                              CTATTTGGTGCAACAGACCATCCACTGGCTCTTCATGGGTTACTCCATGACTGCCTTCTG
                                                                                             CTATTTGGTGCAACAGACCATCCACTGGCTCTTCATGGGTTACTCCATGACTGCCTTCTG
                                  CCTCTTCACGTGGGACAAATGGCTTAAGGTGTATAAATCCATCTATTTCCTTGGCCACAT
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Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6809.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAGO65ZE03_CSO6165_1&cluster=6809.f.
Contact : Feng Liang Email : fliang@llfetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAGO65ZE03_CSO6165_1.
Location/Qualifiers
CATTCAAGAGAGCCCCACCCTGAGCAAGCTGGCCGCCATTACTGTCCTCCAGCCCTTCTA
                                                                                                          CCTGGTCTGCTTCCAGATGGAATTCCTCATTGTTATTGTGGAAAGACAGGCTGCCAGGCT
                                                                                                                                                                                                                            ACTCTCTCAGGGTCTCTCGTTGCTATTCCTGGCCCTCTGGCACGGCCTGCACTCAGGATA 1216
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ilarity 100.0%;
Conservative (
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/dev_stage="fetal"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL LIVER"
/clone_lib="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."
vector 201 g 227 t 4 others
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODM004YH02"
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Pred. No. 2.9e-125;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cgi-bin/cluster.cgi?seq=CSObI070DE08QP1&cluster=6809.f. Contact Feng Liang Email: fllang@llfetech.com URL: http://fulllength.invitrogen.com/InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSODI070DE08QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6809.f
more information about this cluster, see
http://www.genoscope.cns.fr/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---, m.b., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX339313 Homo sapiens PLACENTA COT 25-NORWALIZED Homo clone CSODIO70VJ16 5-PRIME, mRNA sequence.

BX339313
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BP 191 91006 EVRY cedex - France
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Mammalia; Eutheria; Primates;
1 (bases 1 to 1149)
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                                                                                                                                                                                                                                                                     Similarity
                                                                                                          CTGAGCCTTAACAAGTTGGCGACGTCCCTGGGCGCGCTCAGAACAGGCGCTGCGGCTGATC
                                                                                                                                                                                     GAGGGGGACGAGGGGACTGTGGTGGTGGCGGGGGTTCTGCAGTCGGGTTTCCAGGAG
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    ATCTCCATCTTCCTGGGTTACCCCTTTGCTTTTATCGGCATTACCTTTTCTACAAG
                                                                                                                                                                  GAGGGGGACGAGGGGACTGTGGTGGCGCTGGCGGGGGTTCTGCAGTCGGGTTTTCCAGGAG
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                                         ATCTCCATCTTCCTGGGTTACCCCTTTGCTTTGTTTTATCGGCATTACCTTTTCTACAAG
                                                                                   CTGAGCCTTAACAAGTTGGCGACGTCCCTGGGCGCGCTCAGAACAGGCGCTGCGGCTGATC
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                                                                                                                                                                                                                                                                                                                                            /tissue type="PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
gigested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
285 c 285 g 298 t 41 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /moi_type="mRNA"
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|mol_type="mRNA"
                                                                                                                                                                                                                                                                  34.0%;
100.0%;
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                                                                                                                                                                                                                                                                  Score 773; DB 13;
Pred. No. 1.8e-123;
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AGENCOURT 8801447 NIH MGC 129 Mus
5', mRNA Sequence.
BQ917856
BQ917856.1 GI:22332554
                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
cDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMA13734 row: n column: 24
High quality sequence stop: 755.
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 974)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                          Unpublished
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Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
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AGENCOURT_10325398 NIH_MGC_40 Homo
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Similarity 100.0%;
57; Conservative (
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/clone lib="NIH MGC 129"
/clone lib="NIH MGC 129"
/note="Organ: olfactory epithelium; Vector:
pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned
unidirectionally. Primer: Oligo dT. Average insert size
2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: th
is a NIH_MGC Library."
a 260 c 248 g 267 t
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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Best Local Similarity
Matches 751; Conserv
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BU541837
BU541837.1 GI:22
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1 (Dases 1 to 916)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCAGCGGAGGGGACGAGGGGACTGTGGTGGCGCTGGCGGGGGTTCTGCAGTCGGGTTT
CTACCTTCTGGCTGGATACTATTACACTGCCACCGGCAACTACGATATCAAGTGGACAAT
                                                                                                CCTTCGACTAATGGGCCGCACCATCACTGCCGTCCTCACTACCTTTTGCTTTCCAGATGGC
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                                                                        CCTTCGACTAATGGGCCGCACCATCACTGCCGTCCTCACTACCTTTTGCTTCCAGATGGC
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Location/Qualifiers
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/clone="IMAGE:6573588"
/tissue_type="carcinoma, cell line"
/lab host="DH108 (phage-resistant)"
/lab host="DH108 (phage-resistant)"
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/clone_lib="NIH_MGC_40"
/note="Organ: pTostate; Vector: pOTB7; Site_1: XhoI;
/site_2: EcoRI; cDNA made by oligo-dT priming.
Site_2: EcoRI; cDNA made by oligo-dT priming.
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 1.2e-119;
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602726506F1 NIH_MGC_15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1732 row: k column: 02
High quality sequence stop: 776.
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates;
1 (bases 1 to 800)
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BG823157.1 GI:14170744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can
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           /lab_host="DH10B (phage-resistant)"
/clome lib="NH1 MGC 15"
/clome lib="NH1 MGC 15"
/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
61 a 218 c 199 g 222 t
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/tissue_type="adenocarcinoma cell line"
/tissue_type="adenocarcinoma cell line"
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Homo sapiens
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REFERENCE AUTHORS

(bases 1 to 911)
 NIH-MGC http://mgc.nci.nih.gov/ National Institutes.of Health,

Mammalian

Gene

Collection (MGC)

Eukaryota; Metazoa; Mammalia; Eutheria; Homo sapiens

Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.

TITLE

KEYWORDS SOURCE ORGANISM

sapiens (human)

ACCESSION DEFINITION

AGENCOURT 10809550 MAPCL mRNA sequence.
CA489207
CA489207.1 GI:24951998

CA489207

911 | Homo ďď sapiens

mRNA ens cDNA

linear clone I

r EST 14-NOV-IMAGE: 6721545

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM14282 row: n column: 09
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Email: cg
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Tissue Procurement: Kristi A. Egland,
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                                                                                          CCTGGCCCTCTGGCACGGCCTGCACTCAGGATACCTGGTCTGCTTCCAGATGGAATTCCT
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/note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
Insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."

Manuscript submitted."
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/clone="IMAGE:6721545"
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/mol_type="mRNA"
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plate: LLCM1967 row: e column: 20
High quality sequence stop: 677.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
AAAGAACTCTCTCAGGGTCTCTCGTTGCTATTCCTGGCCTCTGGCCACGGCCTGCACTCA 121
                                                                               ATCAACACCAACGCCTGGGTGGCCCGCTACATCTTCAAACGACTCAAGTTCCTTGGAAAT 1151
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                                       ATCAACACCAACGCCTGGGTGGCCCGCTACATCTTCAAACGACTCAAGTTCCTTGGAAAT
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                                                                                                                                                                                                                                    230
                                                                                                                          Conservative
                                                                                                                                                                                                                           /clone="IMAGE:5466619"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH108 (phage-resistant)"
/clone_libe"NIH_MGC_41"
/clone_libe"NIH_MGC_41"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI, cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC_Library."
30 a 313 c 237 g 267 t 6 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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Pred. No. 5.4e-118;
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                                                                                                                                                     AL557774 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED Homo sapiens CDNA clone CSODJ003YA18 5-PRIME, mRNA sequence.

AL557774 AL557774

AL557774.2 GI:31279574

EST.
                                Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Primates; Catarrhini; Ho
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                         Homo
 Unpublished On Feb 15, ;
                                                                                                                                                                                                                                                                                                                                                                                                                    TTTGTATTTTCAGTAGAAACGGGATTTCACCACGTTGGCCAGGCTGGTCTCGAACTCCTG
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 15, 2001 this sequence
                                   and normalization
                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 version replaced
gi:12901710.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6809.f
more information about this cluster, see
http://www.genoscope.cns.fr/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgi-bin/cluster.cgi?seq=CS0DJ003BA09QP1&cluster=6809.f. Contact
Feng Liang Email : filang@lifetech.com VRL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DJ003BA09QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                       TCTGAGCAACAGAAATATGCCATACGTGGTGTTCCTTCCCTGCTGGAAGTTGCTGGTTTC
                                                                                                         AAGCTGATTGGTTTGGCTGTTGACTACTTTGACGGAGGGAAAGATCAGAATTCCCTTGTCC
                                                                                                                                                         TACACTGCCACCGGCAACTACGATATCAAGTGGACAATGCCACATTGTGTTCTGACTTTG
                                                                                                                                                                          TACACTGCCACCGGCAACTACGATATCAAGTGGACAATGCCACATTGTGTTTCTGACTTTG
                                                                                                                                                                                                                            CACCTCTTCCATACCTTTACAGGCCTCTCAATTGCTTATTTTAACTTTGGAAACCAGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA" | FRANA" |
/mol_type="mRNA" |
/db xref="taxon:9606"
/clone="CSODJ003YA18"
/cell_type="T CELL (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_lime="JURKAT"
/cell_lime="JURKAT"
/clone_lime="JURKAT"
/clone_lime="JURKAT"
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Pred. No. 1.1e-116;
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Best Local Similarity
Matches 765; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: LLCM1759 row: j column: High quality sequence stop: 814. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    887 bp m 602733053F1 NIH MGC 43 Homo sapiens mRNA sequence.
BG753831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Ling Hong/Rubin Laboratory
 TTCCTTGGAAATAAAGAACTCTCTCAGGGTCTCTCGTTGCTATTCCTGGCCCTCTGGCAC 1199
                                                                          GCCTCATTCAACATCAACACCAACGCCTGGGTGGCCCGCTACATCTTCAAACGACTCAAG
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                                       GCCTCATTCAACATCAACACCAACGCCTGGGTGGCCCGCTACATCTTCAAACGACTCAAG
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                                                                                                                                                                                                                                                                                       208
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                               /clone="IMAGE:4876525"
/tlissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 43"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT prining. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library. | "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 1.7e-113;
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                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 847)
                                                   found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM11462 row: d column: 17
                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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603045066F1 NIH_MGC_116 Homo
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Location/Qualifiers
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sapiens
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BASE COUNT ORIGIN

Matches

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EST 31-MAY-2003

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                                                GCTGGTGCAGGGAGAGCTGATTGACATACCAGGAAAGATACCAAACAGCAT 727
                                                                                      GCTGGTGCAGGGAGAGCTGATTGACATACCAGGAAAGATACCAAACAGCAT 757
                                                                                                                                                CTCCTACTTCTATGGGGCCTTCTTGGTAGGGCCCCAGTTCTCAATGAATCACTACATGAA
                                                                                                                                                                                       CTCCTACTTCTATGGGGCCTTCTTGGTAGGGCCCCCAGTTCTCAATGAATCACTACATGAA 706
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//Clone lib="NIH MGC 116"
//Clone lib="NIH MGC 116"
//Clone lib="Cryan: pooled colon, kidney, stomach; Vector:
//Clone lib="Cryan: pooled colon, Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH MGC Library."

70 a 236 c 210 g 231 t
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/mol type="mRNA"
/db xref="taxon:9606"
/clone="TMAGE:5185120"
/lab_host="DH10B"
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AL553069 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI072Y019 5-PRIME, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.genoscope.cns.fr/
cgi-bi/cluster.cgi?seq=CSODIO72AH10QP1&cluster=6809.f.
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6809.
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Feb 15, 2001 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODI072AH10QP1.
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                                                                         ACTGCTCAGCCCCCACATCACAGAAGACTATCTCCTCACTGAAGACTATGACAACCACCC
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                                                ACTGCTCAGCCCCCACATCACAGAAGACTATCTCCTCACTGAAGACTATGACAACCACCC
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized
a 273 c 274 g 309 t 57 others
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/db_xref="taxon:9606"
/clone="CSODI072YO19"
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                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1968 row: h column: 07
High quality sequence stop: 666.
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AGENCOURT 6572558 NIH MGC 41
5', mRNA sequence. -
BM553135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
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                                                                        244
                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: (
Location/Qualifiers
                                                                 /clone="IMAGE:5467062"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_41"
/clone_lib="NIH MGC_41"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI, cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

44 a 315 c 254 g 275 t 9 others
                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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sapiens cDNA clone
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                                                  Contact: Robert Strausberg, Email: cgapbs-r@mail.nih.gov Tissue Procurement: NCI
                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 82)
                                                                                                                                                                                                                                                              5', mRNA sequence
BU597281
BU597281.1 GI:232
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AGENCOURT 8966025 NIH MGC 142
                                                                                                         Unpublished
                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                                              Homo sapiens (human)
cDNA Library Preparation: Michael Brownstein Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Agencourt Bioscience Corporation
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Best Local Similarity
Matches 703; Conserv
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Location/Qualifiers
                             GGCGTCTTGCTTTGTCACCCACGCTGGAATGCAGTGGCGGGATCTCAGCTCACCGCAACC 1787
                                                                                                                                                                                                                                                                                                                  TCCCTGGTGGCCTGTGCGGGACTGGTGCAGAAACTACTCGTCTCCCTTTTCACAGCACTC 1607
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GGCGTCTTGCTTTGTCACCCACGCTGGAATGCAGTGGCGGGATCTCAGCTCACCGCAACC
                                                                                               TĠĊĊTĊTĠĊĊĠĠĊĊĂĠĊĊĂAGTĊTTCATTTGGGĠĊĊĂĂĂĠGGĠĂĂĂCTTTTTTTTTGĠĀĠĀĀ 482
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ilarity 100.0%;
Conservative 0
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/tlissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="MIH MGC 142"
/clone_lib="MIH MGC 142"
/note="Wector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
/inte_2: SfiI (ggcgcttcggcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2*, blood - 3.4*, brain - 5.6*, breast - 12.5*, colon - 2*, blood - 3.4*, brain - 5.6*, breast - 12.5*, colon - 2*, blood - 3.4*, brain - 5.6*, lung - 10.8*, NK.cell - 5.2*, vowary - 4*, pharynx - 2.5*, prostate - 4.3*, salivary ovary - 4*, pharynx - 2.5*, prostate - 4.3*, salivary gland - 1.3*, and skin - 2.3*). 5' and 3' adaptors were used in cloning as follows:

5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and 5'-AAGCAGTGGGCCAACAGTG-4T(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the >0.5 kb size fraction (other fractions present in NIH MGC 141).

Library created in the laboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 2e-111;
0; Mismatches 0;
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Search completed: November 22, 2003, 12:02:52 Job time : 4745 secs

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Result
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                                                                                                                                                                                                                                                                                   results predicted by chance to have a to the score of the result being printed,
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                    AAC88075
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AAZ50889
ABK84420
ABN96918
ABL64098
AAF25159
  AAS70385
                                                                                                                                                                                                                                  SUMMARIES
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## ALIGNMENTS

RESULT 1 AAC88075

AAC88075;

AAC88075 standard; cDNA; 2273 BP

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PR XXX
                                                                                                                                                                                                                                                                                      Human; FLEXHT; full-length molecules expressed in human tissue; diagnosis; gene expression; genetic linkage; genetic variability; antianaemic; anticonvulsant; antiarteriosclerotic; immunomodulatory; cytostatic; antiasthmatic; antianflammatory; hepatotropic; antidiabetic; anti-gout; antithyroid; neuroprotective; antiarthritic; osteopathic; antipsoriatic; antirheumatic; antiulcer; gene therapy; anaemia; gout;
                                                                                                                                                                                                                             epilepsy; arteriosclerosis; atherosclerosis; developmental discancer; immunological disorder; asthma; bronchitis; cirrhosis; Crohn's disease; diabetes mellitus; Grave's disease; multiple
                                                                                                                                                                                                                                                                                                                                                                                                                              Human FLEXHT-6 nucleotide sequence SEQ ID NO:61.
14-MAY-1999;
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                                  12-MAY-2000; 2000WO-US13299
                                                                             23-NOV-2000
                                                                                                               WO200070047-A2
                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                          ulcerative colitis; ss.
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99US-0311894.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC88070 to AAC88124 encode the 55 FLEXHT (full-length molecules expressed in human tissues) proteins given in AAB36579 to AAB3633. The present invention describes an isolated polypeptide (A) comprising an amino acid sequence selected from one of 55 amino acid sequences 42-876 residues in length, corresponding to FLEXHT-1 to FLEXHT-55, a 90 % identical sequence, and a biologically active or immunogenic fragment of the sequence. The FLEXHT proteins can have antianaemic, anticonvulsant,
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P-PSDB; AAB36584.
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                                                TGTGTATTGTGCTTCAGTTCCTCATCCTTCGACTAATGGGCCGCACCATCACTGCCGTCC
                                                                                                            CCTTTACAGGCCTCTCAATTGCTTATTTTAACTTTTGGAAAACCAGCTCTACCACTCCCTGC
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                               TGTGTATTGTGCTTCAGTTCCTCATCCTTCGACTAATGGGCCGCACCATCACTGCCGTCC
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                                                                                                    Human; hydrophobic protein; secretory protein; membrane protein; sepsis; tumour inhibition; immune deficiency; autoimmune disorder; anaemia; burn infectious disease; cancer; ulcer; periodontal disease; coagulation; Parkinson's disease; fertility; immune response; thrombosis; ss.
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CC ARF25159 represents a shorter version of the present sequence. The protein possesses a hydrophobic domain and so is a secretory protein cor a membrane protein. The protein is used as an antigen to prepare antibodies. The polynucleotide sequence is useful as a source of probes cor antibodies. The polynucleotide sequence is useful as a source of probes cor genetic diagnosis. It is also useful for producing the protein cor in large quantities and for gene therapy. The enkaryotic cells are used for detecting the receptors or ligands corresponding to the protein and cor for detecting small novel pharmaceuticals. The antibodies are also used for detection, quantification and purification of the proteins both the sources or supplements. The protein may have cytokine and cell cortein and polynucleotide may be used in research or as nutritional corresponding to the protein sources or supplements. The protein may have cytokine and cell cortivity, hematopoiesis regulating activity, timmune stimulating or suppressing activity, through activity, hemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity and tumour inhibition activity. It may therefore may be used to threat inmune deficiencles resulting from autoimmune disorders or infectious diseases, cancer, sepsis, anaemias, burns and ulcers, cor immune response and enhance coagulation or inhibit thrombosis.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 120-124; 151pp; English.
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P-PSDB; AAB31669.
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receptor-associated protein cDNA from Incyte clone 2906971

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AAZSOB Human receptor-associated protein; HRAP; Incyte clone 2906971; cytostatic; immunomodulatory; antiinflammatory; cardiant; antianaemic; antiarteriosclerotic; hepatotropic; antiarthritic antirheumatic; antiasthmatic; osteopathic; antiallergic; antidiabetic; dermatological; neuroprotective; diagnosis; treatment; prevention; reproductive disorder; cardiovascular; cell proliferative; autoimmune; inflammatory; allergy; gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS; arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis; multiple sclerosis; irritable bowel syndrome; ss.

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Best Local Similarity
Matches 2186; Conserv
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treatment and prevention of cell proliferative, autoimmune,
inflammatory, reproductive, cardiovascular, and gastrointestinal
disorders -
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             adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease;
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                                        cardiac reperfusion
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Conservative

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CC (GCA), by detecting the level of expression of gene(s) (GS) identified by CC (GCA), by detecting the level of expression of gene(s) (GS) identified by CC the expression level to an expression of Gs is indicative of GCA. CC Also included are modulating (M2) GA by contacting GC with an agent capable of modulating (M2) GA by contacting GC with an agent capable of modulating GCA or an inflammation (especially CC chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the treating (M3) an inflammation (especially CC chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression of the gene is indicative of inflammation; (M5) an inflammation (especially creating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the creating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having GCA inflammation with an agent that modulates the expression of gene(s) cromages in a subject capable of modulating GCA in an inflammation (especially chronic) or in a tissue, and capable of modulating GCA in an inflammation (especially chronic) or in a tissue, and inflammation (especially chronic) or in a tissue, an allergic cresponse in a subject capable of modulating GCA in a subject capable of modulating GCA in a subject capable of modulating GCA in a subject capable of modulating GCA in a subject capable of modulating GCA in a subject capable of modulating GCA in a subject capable of modulating GCA in a subject capable of modulating GCA in a subject capable of modulating GCA in a subject capable of modulating GCA in a subject capable of modulating GCA in a subj
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                                                                                                                       of the printed specification, but format directly from WIPO at
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Peres-Da-Silva S,
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Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease st disease progression; drug toxicity; drug efficacy; drug metabolism.
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The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from thepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cycostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, converse that can be used to monitor disease states, disease progression, converse that can be used to monitor disease states, disease progression, converse that can be used to monitor disease states, disease progression, converse the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO cat figure in the patient of the printed specification, but was obtained in electronic format directly from WIPO cat figure in the patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO cat figure in the patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO cat figure in the patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO cat figure in the patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO cat figure in the patient did not form part of the printed specification.
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18-SEP-2000; 2000US-234034P.
20-SEP-2000; 2000US-234034P.
20-SEP-2000; 2000US-234953P.
22-SEP-2000; 2000US-234953P.
25-SEP-2000; 2000US-234923P.
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29-SEP-2000; 2000US-237773P.
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20-OCT-2000; 2000US-2377295P.
20-OCT-2000; 2000US-23737694P.
20-OCT-2000; 2000US-237604P.
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cytostatic; gene therapy; antineoplastic; Wilm's tumour;
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h; lung; prostate; pancreas; carcinoma; antitumour; cancero
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical eagent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a cresult of M1, and the data is sufficient to convey the chemical constructure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, scomach, lung, thyroid, cosophageal, ovarian, kidney, prostate or pancreatic cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
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The present sequence encodes a human protein with hydrophobic domains. ARF25169 represents a longer version of the present sequence. The protein possesses a hydrophobic domain and so is a secretory protein or a membrane protein. The protein is used as an antigen to prepare antibodies. The polynucleotide sequence is useful as a source of probes for genetic diagnosis. It is also useful for producing the protein in large quantities and for gene therapy. The eukaryotic cells are used for detecting the receptors or ligands corresponding to the protein and

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Best Local Similarity
Matches 1461; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for detecting small novel pharmaceuticals. The antibodies are also used for detection, quantification and purification of the proteins. Both the protein and polynucleotide may be used in research or as nutritional sources or supplements. The protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, hematopoiesis regulating activity, tissue growth activity, activiny, hinhibin activity, receptor/ligand activity, and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity and tumour inhibition activity. It may therefore may be used to infectious diseases, cancer, sepsis, anaemias, burns and ulcers, periodontal disease, Parkinson's disease, induce fertility, improve immune response and enhance coagulation or inhibit thrombosis.
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RESULT 8
AAS70385
31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                              30-MAR-2001; 2001WO-US08631
                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                     DNA encoding novel human diagnostic protein #6189
                                                                                                                                                                         13-FEB-2002
                                                                                                                                                                                                              AAS70385
                                                                 11-OCT-2001.
                                                                                    WO200175067-A2
(HYSE-) HYSEQ INC
                                                                                                                                                                                                              standard;
                                                                                                                                                                         (first entry)
                                                                                                                                                                                                              CDNA; 1867
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forensic;

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CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polymucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
cc specification, but was obtained in electronic format directly from WIPO
cc at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes.
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CC The invention relates to novel isolated lung cancer antigen CC polynucleotides (I) and polypeptides (II). (I) and (II) are used to CC prevent, treat or ameliorate a medical condition in e.g. humans, mice, CC rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) are CC also used in diagnosing a pathological condition or susceptibility to a CC pathological condition, in particular, lung cancer. The antibodies to CC (II) can also be used in alleviating symptoms associated with the CC clinked immunosorbent assays (ELISA) bisorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthirtis, CC hyperproliferative disorders e.g. neoplasms of the breast or liver, CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infections. The polypeptides can also be CC used to aid wound healing and epithelial cell proliferation, to prevent CC supporting cell culture of primary tissues, to regenerate tissues and in C cenebrasis. AASJOSBO-AASJOSBS represent novel human lung cancer antigen CC coding sequences, PCR primers and related sequences of the invention. CC printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; lung cancer; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; autoimmune disease; rheumatoid arthritis; neoplasm; hyperproliferative disorder; cardiovascular disorder; anglogenesis; nervous system disorder; Alzheimer's disease; infection; skin aging; nervous system disorder; Alzheimer's disease; infection; skin aging;
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Human; respiratory antigen; respiratory disorder; throat disorder; lung disorder; nose disorder; lung cancer; gene therapy; cytostatic; anti allergic; anti asthmatic; anti inflammatory; olfactory;

respiratory active; ds

Genomic sequence #541 encoding

for novel human respiratory antigen.

07-NOV-2001

(first

entry)

AAS28701

standard;

DNA;

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2000US-0235484. 2000US-0235484. 2000US-0235834.	2000US-0234997.	2000US-0234223. 2000US-0234274.	2000US-0233065.	2000US-0233063.	2000US-0232401.	2000US-0232399.	200005-0232398.	2000US-0231968.	2000US-0232081.	2000US-0232080.	2000US-0231414.	2000US-0231244.	2000US-0231243.	2000US-0231242.	2000US-0230437.	2000US-0229513.	2000US-0229509.	2000US-0229344.	2000US-0229343.	2000US-0229287.	2000US-0221009.	2000US-0227182.	2000US-0226868.	2000US-0226681.	2000018-0226279	2000US-0225758.	2000US-0225757.	2000US-0225447.	2000US-0225268.	2000US-0225267.	2000US-0225214.	2000US-0225213.	2000US-0224519.	2000US-0220964.	2000US-0220963.	2000008-0217496.	2000US-0217487.	2000US-0216880.	2000US-0215135.	2000US-0214886.	2000US-0205515.	2000US-0198123.	2000US-0189874.	00US-018635	00US-018466	2 2		2001WO-US01333.		11.	
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The present invention relates to the isolation of novel human creapiratory antigens (AAU17685-AAU17975), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the cinvention are useful for preventing, treating and/or prognosing disorders related to the respiratory system including throat disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis), clung disorders e.g. pneumonia, allergic disorders e.g. asthma, pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of the respiratory tissues e.g. lung cancer. The polymucleotide sequences of the invention are useful in gene therapy and antisense therapy.

CC AAS28161-AAS28764 represent genomic sequences encoding for novel thuman respiratory antigens.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fifth the printed specification, but was obtained pot_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amyotrophic lateral sclerosis; infectious disease; viral infection; bacterial infection; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  constant region; immunotherapy; gene therapy; lung disorder; leukopenia;
small cell lung cancer; squamous cell carcinoma; adenocarcinoma; asthma;
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The invention relates to an isolated lung cancer related polypeptide its covariants, allelic variants or homologues. The polypeptide and its nucleic acid are useful for preventing, treating, or ameliorating a medical condition in a mammalian subject, for diagnosing a pathological condition (c) or a susceptibility to a pathological condition in the nucleic acid or determining the presence or absence of mutation in the nucleic acid or condition in the polypeptide in a biological condition and diagnosing a pathological condition based on the complex of the polypeptide or the polypeptide and diagnosing a pathological condition based on the complex of the polypeptide or the polypeptide are useful for detecting, treating, preventing and/or prognosing diagorders of the lung, such as small cell lung cancer, non-cell carcinoma, adenocquamous cell carcinoma, adenocarcinoma, cell carcinoma or lung cancer metastasis. The polypeptide, its antibodies or its polynucleotide are also useful for detecting, treating, preventing and/or prognosing diagorders syndrome; hyperproliferative disorders e.g. and/or prognosing respiratory disorders e.g. non-allergic rhinitis and cancer metastasis. The polypeptide, its antibodies or its polynucleotide are also useful for detecting, treating, preventing candult respiratory disorders e.g. non-allergic rhinitis and candult respiratory disorders e.g. non-allergic rhinitis and candult respiratory disorders e.g. non-allergic rhinitis and candult respiratory disorders e.g. anaphylaxis and asthma; concerns and leukopenia; allergic reactions; however allergic rhinitis and disorders e.g. anaphylaxis and asthma; concerns and leukopenia; allergic reactions e.g. anaphylaxis and asthma; concerns and secondary of the polypeptide and sorders e.g. anaphylaxis and kidney failure; cardiovascular disorders e.g. arrhythmia and myocardial inflammatory disorders e.g. arrhythmia and myocardial inflammatory disorders e.g. arrhythmia and myocardial system disorders e.g. Aldison's concerns and concerns and concerns a
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RUBEN S M.
BARASH S C.
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and/or prognosing lung, respiratory, hyperproliferative,
tem, cardiovascular endocrine or gastrointestinal disorders
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                                                                                                                  CAGGAATCTATTGTGTTTTTCTTCTGCCAATTTACTATGATTGTGTATGTGCCGCTACCA
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Pred. No. 3e-300;
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ABA15665 standard; DNA; 32174

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system related polynucleotide SEQ ij ŏ

Human; nootropic; neuroprotective; cytostatic; dermatological; vi immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vul antiparkinsonian; antisickling; antianaemic; antiarthritic; cance antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal antiarthritic; cancer;

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Homo sapiens W0200159063- 16-AUG-2001 17-JAN-2000 24-FEB-2000 24-FEB-2000 16-MAR-2000 11-JAN-2000 11-JAN-2000 11-JAN-2000 11-JAN-2000 11-JUL-2000 11-J
A2.  2001WO-US01334. 2000US-019065. 2000US-0180628. 2000US-01884664. 2000US-0186350. 2000US-0186350. 2000US-0186350. 2000US-0198123. 2000US-0198123. 2000US-0198123. 2000US-0215135. 2000US-0215135. 2000US-0216880. 2000US-0214886. 2000US-0214886. 2000US-0214886. 2000US-0214886. 2000US-0224518. 2000US-0224518. 2000US-0225214. 2000US-0225214. 2000US-0225214. 2000US-0225214. 2000US-0225214. 2000US-0225214. 2000US-0225214. 2000US-0225214. 2000US-0225214. 2000US-0225266. 2000US-0225266. 2000US-0225266. 2000US-0225275. 2000US-0225266. 2000US-0225266. 2000US-0225214. 2000US-0225214. 2000US-0225214. 2000US-0225214. 2000US-0225214. 2000US-0225214. 2000US-0225214. 2000US-0225214. 2000US-0225214. 2000US-0225214. 2000US-0225214. 2000US-0225214. 2000US-0225214. 2000US-02331414. 2000US-02331414. 2000US-02331414. 2000US-02331414. 2000US-0233239. 2000US-0233239. 2000US-0233239. 2000US-0233239. 2000US-02332401. 2000US-02332401. 2000US-02334223. 2000US-02334223. 2000US-023344223. 2000US-0234497.
nephrotropic; gene
therapy; vaccine;
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25-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 20-OCT-2000 20-OCT
2000US-0234998. 2000US-0235844. 2000US-0235844. 2000US-0235834. 2000US-023638. 2000US-023638. 2000US-023638. 2000US-023638. 2000US-023638. 2000US-023638. 2000US-023638. 2000US-0237039. 2000US-0237039. 2000US-02497175. 2000US-0249718. 2000US-0246477. 2000US-0246477. 2000US-0246477. 2000US-0246477. 2000US-0246477. 2000US-0246477. 2000US-0246477. 2000US-0246477. 2000US-0246477. 2000US-0246477. 2000US-0246477. 2000US-024628. 2000US-024921. 2

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(ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, altergies, autoimmune hammend and their face multiple sclerosis, rheumatoid arthritis and ulcerative colities, (c) cardiovascular disorders uch as myocardial ischaemias; (d) wound healing; (e) neurological disease e.g. cerebral anoxia and epilepsy, and (f) infectious diseases such as viral, bacterial, fungal and parasitic infectious.
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                                                                                                                                       GGCTGGTCTCGAACTCCTGACCGCAAGTGATCCACCCGCCTCCGCCTCCCAAAGTGCTGG 1972
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              GGGGCTCACATCTCCCCCTGATTCCCCCATGCACATTGCCTTATCTCTCCCCATCTAGC
                                                                               GATTACAGGCGTGAGCCACCGTGCCCCGGCCCAAAGGGGGAAACTCTTGTGGGAGGAGCAGA
                                                                                                                       GGCTGGTCTCGAACTCCTGACCGCAAGTGATCCACCCGCCTCCGCCTCCCAAAGTGCTGG
                                                                                                                                                                                  CCACCATGCCCAGCTAATTTTTGTATTTTCAGTAGAAACGGGATTTCACCACGTTGGCCA
                                                                                                                                                                                                                                           CTCCTGGGTTCAAGTGATTTTCCTGCCTCAGCCTCCCAAGTAGCTGGGAATACAGGCACG
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30-JUN-2000;
07-JUL-2000;
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11-JUL-2000;
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14-JUL-2000;
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19-MAY-2000;
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02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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2000US-0184664.
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                                                                                                                                                                                 disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic
useful f
                                                                                                                                                                                                                                                                                                                        The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hamalytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                                                                                                                           Sequence 32174 BP; 8747 A; 7064 C; 6837
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1613 CCCCAGAGCAGAGAATGGAAAAGCCAGGGAGGTGGAAGATCGATGCTTCCAGCTGTGCCT 1672
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for preventing, diagnosing and/or treating nervous system
s and metastases -
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                                                 GGTGGCCTGTGCGGGACTGGTGCAGAAACTACTCGTCTCCCCTTTTCACAGACTCCCTTTG
                              GGTGGCCTGTGCGGGACTGGTGCAGAAACTACTCGTCTCCCTTTTCACAGCACTCCTTTG
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2000US-0251479.
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         CCTTGGAACTGTATTAGATAAAATCACTTCTGTTTGTTCAGTTTTTCA
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing, (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. Sequence 32174 BP; 8747 A; 7064 C; 6837 G; 8001 T; 1525 other; GGTGGCCTGTGCGGGACTGGTGCAGAAACTACTCGTCTCCCTTTTCACAGCACTCCTTTG GATTACAGGCGTGAGCCACCGTGCCCGGCCCAAAGGGGAAACTCTTTGTGGGAGGAGCAGA CACCATGCCCAGCTAATTTTTGTATTTTCAGTAGAAACGGGATTTCACCACGTTGGCCA CCCCAGAGCAGAGAATGGAAAAGCCAGGGAGGTGGAAGATCGATGCTTCCAGCTGTGCCT CCCCAGAGCAGAAATGGAAAAGCCAGGGAGGTGGAAGATCGATGCTTCCAGCTGTGCCT CAGGAATCTATTGTGTTTTTTCTTCTGCCAATTTACTATGATTGTGTGTATGTGCCGCTACCA GGGGCTCACATCTCCCCCTCTGATTCCCCCCATGCACATTGCCCTTATCTCTCCCCCATCTAGC GATTACAGGCGTGAGCCACCGTGCCCGGCCCAAAGGGGAAACTCTTGTGGGAAGGAGCAGA CTCCTGGGTTCAAGTGATTTTCCTGCCTCAGCCTCCCAAGTAGCTGGGAATACAGGCACG CTTGCTTTGTCACCCACGCTGGAATGCAGTGGCGGGATCTCAGCTCACCGCAACCTCCAC GGTGGCCTGTGCGGGACTGGTGCAGAAACTACTCGTCTCCCTTTTCACAGCACTCCTTTG CAGGAATCTATTGTGTTTTTCTTCTGCCAATTTACTATGATTGTGTATGTGCCGCTACCA GGGGCTCACATCTCCCCTCTGATTCCCCCCATGCACATTGCCTTATCTCTCCCCCATCTAGC GGCTGGTCTCGAACTCCTGACCGCAAGTGATCCACCCGCCTCCGCCTCCCAAAGTGCTGG GGCTGGTCTCGAACTCCTGACCGCAAGTGATCCACCCGCCTCCGCCTCCCAAAGTGCTGG CCACCATGCCCAGCTAATTTTTGTATTTTCAGTAGAAACGGGATTTCACCACGTTGGCCA 1912 CTCCTGGGTTCAAGTGATTTTCCTGCCTCAGCCTCCCAAGTAGCTGGGAATACAGGCACG CTTGCTTTGTCACCCACGCTGGAATGCAGTGGCGGGATCTCAGCTCACCGCAACCTCCAC Score 708; DB 22; ; Pred. No. 2.8e-300; 0; Mismatches 0; GGAGAGGGGTGCAAGGCCCTGCCTGCTCCACTTTTTCTA 0; Length 32174; Indels 2260 0; Gaps 1732 2032 1792 1672 1612 26791 2212 2673 2152 26671 2092 26551 1972 2649: 26431 1852 26371 26311 26251 26191 2661 0

26839

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RESULT 15
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26-JUL-2000;
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07-JUL-2000;
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          2000US-0216880.
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2000US-0229963.
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2000US-0225267.
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25-SEP-2000;
26-SEP-2000;
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20-CC
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases
                                                                                                                                                                                                                                                                                                                                                                  Sequence 32174 BP; 8001 A; 6837 C; 7064 G; 8747 T; 1525 other;
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                                                                                                                                                                                                                                       GGTGGCCTGTGCGCGGACTGGTGCAGAAACTACTCGTCTCCCTTTTCACAGCACTCCTTTG
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                                                 CTTGCTTTGTCACCCACGCTGGAATGCAGTGGCGGGATCTCAGCTCACCGCAACCTCCAC
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ਲ ੱ	5803 CTCCTGGGTTCAAGTGATTTTCCTGCCTCAGCCTCCAAGTAGCTGGGAATACAGGCACG 5744	44
γ	1853 CCACCATGCCCAACTTAATTTTTGTATTTTCAGTAGAAACGGGATTTTCACCACGTTGGCCA 19	1912
¥	5743 CCACCAIGCCCAGCTAATTTTTGTATTTTCAGTAGAAACGGGGATTTCACCACGTTGGCCA 5684	84
¥	1913 GGCTGGTCTCGAACTCCTGACCGCAAGTGATCCACCCGCCTCCGCCTCCCAAAGTGCTGG 19	1972
¥	5683 GGCTGGTCTCGAACTCCTGACCGCAAGTGATCCACCCGCCTCCGAAAGTGCTGG 5624	24
γ	1973 GATTACAGGCGTGAGCCACCGTGCCCGGCCCAAAGGGGAAACTCTTGTGGGAGGAGCAGA 20	2032
ъ	5623 GATTACAGGCGTGAGCCACCGTGCCCGGCCCAAAGGGGAAACTCTTGTGGGAGGAGCAGA 55	5564
Ϋ́	2033 GGGGCTCACATCTCCCCCTCTGATTCCCCCATGCACATTGCCCTTATCTCTCCCCATCTAGC 20	2092
Ъ	5563 GGGGCTCACATCTCCCCTCTGATTCCCCCATGCACATTGCCTTATCTCTCCCCCATCTAGC 5504	0.4
γ	2093 CAGGAATCTATTGTGTTTTTCTTCTGCCAATTTACTATGATTGTGTATGTGCCGCTACCA 21	2152
쓩	5503 CAGGAATCTATTGTGTTTTTCTTCTGCCAATTTACTATGATTGTGTATGTGCCGCTACCA 5	5444
Υζ	2153 CCACCCCCCCATGGGGGGGTGGAGAGGGGTGCAAGGCCCTGCCTG	2212
Ъ	5443 CCACCCCCCATGGGGGGTGGAGAGGGGTGCAAGGCCCTGCCTG	5384
¥	2213 CCTTGGAACTGTATTAGATAAAATCACTTCTGTTTGTTCAGTTTTTCA 2260	
ъ	5383 CCTTGGAACTGTATTAGATAAAATCACTTCTGTTTGTTCAGTTTTTCA 5336	

Search completed: November 22, 2003, 10:43:39 Job time : 603 secs

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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

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14 US-10-091-548-91
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 Sequence 26, Appl
Sequence 31415, Ap
Sequence 1135, Ap
Sequence 1135, Ap
Sequence 91, Appl
Sequence 1135, Ap
Sequence 1134, Ap
Sequence 2545, Ap
Sequence 232, Appl
Sequence 232, Appl
Sequence 90, Appl
Sequence 90, Appl
Sequence 10135, A
Sequence 10135, A
Sequence 10135, A
Sequence 10135, A
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US-09-938-803-26
; Sequence 26, Application U
; Patent No. US20020076762A1
; GENERAL INFORMATION:

Application US/09938803

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Sequence 26058,	Sequence 26058,	æ	Sequence 142952	Sequence 104432,	Sequence 325526		10443	180	9 119	Sequence 292, App	185		Sequence 105780,			142951	Sequence 8552, Ap		6702	Sequence 13, App	1369,	œ	Sequence 271, Ap	æ	Sequence 26257,	Sequence 22426,	Sequence 11899,	·

## ALIGNMENTS

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APPLICANT: Yue, Henry
APPLICANT: Tang, Y. Tom
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Reddy, Roopa
APPLICANT: Reddy, Roopa
APPLICANT: Yang, Junming
APPLICANT: Yang, Junming
APPLICANT: Arimzai yalda
TITLE OF INVENTION: FULL-LENGTH EXPRESSED GENETIC MARKERS
FILE REFERENCE: PF-0695 US
CURRENT APPLICATION NUMBER: US/09/938,803
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 09/311,894
PRIOR FILING DATE: 1999-05-14
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; NAME/KBY: misc_feature
; OTHER INFORMATION: Incyte Clone 1928920
US-09-938-803-26
                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PERL Program
SEQ ID NO 26
LENGTH: 2273
TYPE: DNA
                                                                                                                                                    Query Match 100.0%; Score 2273; Best Local Similarity 100.0%; Pred. No. 0; Matches 2273; Conservative 0; Mismatches
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61 GGGCTCCCGGAGTTAAGATGGCGTCCTCAGCGGAGGGGGACGAGGGGGACTGTGGTGGCGC 120
                                                                                           DB 9; Length 2273;
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1 TCG 1	Qy Db	841 ATCTCCTCACTGAAGACTATGACAACCCCTTCTGGTTCCGCTGCATGTACATGCTGA 900
1861 CCCAGCTAATTTTTGTATTTTCAGTAGAAACGGGATTTCACCACGTTGGCCAGGCTGGTC 1861 CCCAGCTAATTTTTGTATTTTCAGTAGAAACGGGATTTCACCACGTTGGCCAGGCTGGTC	9	AGCTGATTGACATACCAGGAAAGATACCAAAACAGCATCATTCCTGCTCTCAAGCGCCTGA 7 GTCTGGGCCTTTTCTACCTAGTGGGCTACACACACTGCTCAGCCCCCACATCACAGAAGACCT 8
	Qy Db	661 GGGCCTTCTTGGTAGGGCCCCAGTTCTCAATGAATCACTACATGCAGCTGCTGCAAGCGGCCTGA 780  721 AGCTGATTGACATACCAGGAAAGATACCAAACAGCATCATTCCTGCTCTCAAGCGCCCTGA 780
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1441 ATTTCCTTGGCCACATCTTCTTCCTGAGCCTACTATTCATATTGGCTTATATTCACAAAG	g 89	TGTGTATTGTGCT
1 CCA	Qy Db	301 CCTTTACAGGCCTCTCAATTGCTTATTTTAACTTTGGAAACCAGCTCTACCACTCCCTGC 360
21 TCC	D	241 CTTTGTTTTATCGGCATTACCTTTTCTACAAGGAGACCTACCT
61 GACAGGCTG	DB 42	181 TGGGCGCGTCAGAACAGGCGCTGCGGCTGATCATCTCCATCTTCCTGGGTTACCCCCTTTG 240
ol GCCTGCACTCAGGA	S B 4	121 TGGCGGGGTTTCGCAGTCGGGTTTCCAGGAGCTGAGCCTTAACAAGTTGGCGACGTCCC 180
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CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT PILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR PILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3415
LENGTH: 1842
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Best Local Similarity
Matches 1842; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Genbank Accession No. -09-880-107-3415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-W0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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                                                    AGCCCCACATCACAGAAGACTATCTCCTCACTGAAGACTATGACAACCACCCCTTCTGG
                                                                                                   ATTCCTGCTCTCAAGCGCCTGAGTCTGGGCCTTTTCTACCTAGTGGGCCTACACACTGCTC
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TCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAAGGGGAAACTCTT
                                                          CACCACGTTGGCCAGGCTGGTCTCGAACTCCTGACCGCAAGTGATCCACCCGCCTCCGCC
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US-09-764-860-1135/c
US-09-764-860-1135/c
Sequence 1135, Application US/09764860
Patent No. US20020094953A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE: OF INVENTION: Nucleic Acids, Proteins, and FILE REFERENCE: PC008
CURRENT APPLICATION NUMBER: US/09/764,860
CURRENT FLING DATE: 2001-01-17
Prior application data removed - consult PALM or NUMBER: OF SEQ ID NOS: 1198
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1135
LENGTH: 7461
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-860-1135
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Pred. No. 2.8e-209;
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Prior application data removed - co
NUMBER OF SEQ ID NOS: 137
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SEQ ID NO 91
LENGTH: 7461
TYPE: DNA
ORGANISM: Homo sapiens
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Patent NO. US20020173454A1
GEMERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA122
CURRENT APPLICATION NUMBER: US/09/764,904
CURRENT FILING DATE: 2001-01-17
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Best Local Similarity 99.4%;
Matches 711; Conservative
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US-10-091-548-91/c
; Sequence 91, Application US/10091548
; Publication No. US20030049703A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 711; Conserv
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA122CI
CURRENT APPLICATION NUMBER: US/10/091,548
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 137
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RESULT 7
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CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 09/764,860
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
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APPLICATION NUMBER: 60/225,757
FILING DATE: 2000-08-14
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FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/251,869
FILING DATE: 2000-12-08
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APPLICATION NUMBER: 60/225,267
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APPLICATION NUMBER: 60/216,647
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OR APPLICATION NUMBER: 60/251,868
OR FILING DATE: 2000-09-01
OR APPLICATION NUMBER: 60/234,997
OR FILING DATE: 2000-09-01
OR APPLICATION NUMBER: 60/234,997
OR FILING DATE: 2000-09-01
OR APPLICATION NUMBER: 60/229,345
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OR FILING DATE: 2000-09-01
OR APPLICATION NUMBER: 60/229,387
OR APPLICATION NUMBER: 60/23,287
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OR APPLICATION NUMBER: 60/23,31,413
OR APPLICATION NUMBER: 60/23,413

FILING DATE: 2000-09-05 APPLICATION NUMBER: 60/236,367 FILING DATE: 2000-09-29

2000-09-05

DR FILING DATE: 2000-09-29

DR APPLICATION NUMBER: 60/241,785

DR FILING DATE: 2000-10-20

DR APPLICATION NUMBER: 60/244,617

DR APPLICATION NUMBER: 60/225,268

APPLICATION NUMBER: 60/236,327

FILING DATE: 2000-10-20 APPLICATION NUMBER: 60/249,299

NUMBER: 60/241,809

FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/236,369
FILING DATE: 2000-09-29
APPLICATION NUMBER: 60/224,519

PRIOR PRIOR

OR APPLICATION NUMBER: 60/237,039
OR FILING DATE: 2000-10-02
OR APPLICATION NUMBER: 60/237,038
OR APPLICATION NUMBER: 60/236,370
OR FILING DATE: 2000-09-29
OR APPLICATION NUMBER: 60/236,370
OR FILING DATE: 2000-10-02
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OR APPLICATION NUMBER: 60/237,037
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OR APPLICATION NUMBER: 60/237,040
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/239,935
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OR APPLICATION NUMBER: 60/239,937
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OR APPLICATION NUMBER: 60/241,787
OR FILING DATE: 2000-10-13
OR APPLICATION NUMBER: 60/241,787
OR APPLICATION NUMBER: 60/241,787
OR APPLICATION NUMBER: 60/246,474
OR FILING DATE: 2000-11-08
OR APPLICATION NUMBER: 60/246,532
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OR APPLICATION NUMBER: 60/226,681
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Sequence 158, Application US/09908711
Patent No. US20020045330A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PA128
CURRENT APPLICATION NUMBER: US/09/908,711
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US/09/101360
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US/07/64,867
PRIOR APPLICATION NUMBER: US/07/64,867
PRIOR APPLICATION NUMBER: US/07/64,867
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01344
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PRIOR APPLICATION NUMBER: US01/0134
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01320
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PRIOR APPLICATION NUMBER: US01/01349
PRIOR APPLICATION NUMBER: US01/01349
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01239
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PRIOR APPLICATION NUMBER: 09/764,869
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: US01/01340
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,874
PRIOR APPLICATION NUMBER: US01/0134
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01334
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,898 SOFTWARE: Pai SEQ ID NO 158 TYPE: DNA ORGANISM: FEATURE: PRIOR FILING DATE: PRIOR APPLICATION N PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR NUMBER OF SEQ ID LENGTH: 32174 APPLICATION NUMBER: 09/764,892 FILING DATE: 2001-01-17 APPLICATION NUMBER: US01/01345 FILING DATE: 2001-01-17 APPLICATION NUMBER: US01/01339 APPLICATION NUMBER: 09/764,888 FILING DATE: 2001-01-17 APPLICATION NUMBER: 60/209 FILING DATE: 2001-01-17 APPLICATION NUMBER: 09/764,891 FILING DATE: 2001-01-17 APPLICATION NUMBER: US01/01354 FILING DATE: 2001-01-17 APPLICATION NUMBER: 09/764,905 APPLICATION NUMBER: US01/01329 Patentin NOS: 167 2000-06-07 .

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OTHER INFORMATION: n e
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Pred. No. 7.2e-209;
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RESULT 10
US-09-764-817-2645/c
; Sequence 2645, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodie;
FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT PILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wra
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 2645
; LENGTH: 32174

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Matches 711; Conservative
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Pred. No. 7.2e-209;
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GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, an FILE REFERENCE: PA122

CURRENT APPLICATION NUMBER: US/09/764,904

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM of NUMBER OF SEQ ID NOS: 137

SOFTWARE: PATENTIN Ver. 2.0

SOFTWARE: PATENTIN Ver. 2.0
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33		; OTHER INFORMATION: n equals a,t,g, or c; NAME/KEY: SITE; LOCATION: (29387); LOTHER INFORMATION: n equals a,t,g, or c; NAME/KEY: SITE	n equals a,t,g, or	a a	OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: SITE LOCATION: (29382) OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: SITE					: SITE : (29371) : (29371) FORMATION: : SITE : SITE	a,t,g, or a,t,g, or	

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Pred. No. 7.2e-209;
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US-09-64-891-10135 ; Sequence 10135, Application US/ ; Publication No. US20030077808A1 ; GENERAL INFORMATION:

US/09764891

Proteins,

and

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Protei
FILE REFERENCE PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM NUMBER OF SEQ ID NOS: 10231 SOFTWARE: PatentIn Ver. 2.0 ខ្ព file wrapper

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SEQ ID NO 10135
LENGTH: 32174
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LOCATION: (1317)
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RESULT 15  US-09-764-891-10179/c US-09-764-891-10179/c US-09-764-891-10179, Application US/09764891  Publication No. US20030077808A1  ; GENERAL INFORMATION: APPLICANT: Rosen et al.  ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  ; FILE REFERENCE: PC006  ; CURRENT APPLICATION NUMBER: US/09/764,891  ; CURRENT FILING DATE: 2001-01-17  Prior application data removed - consult PALM or file wrapper  ; NUMBER OF SEQ ID NOS: 10231  ; SOFTWARE: Patentin Ver. 2.0  ; SEQ ID NO 10179  ; LENGTH: 32174  ; TYPE: DNA	2206 TITTCTACCTTGGAACTGTATTAGATAAAATCACTTCTGTTTGAGTTTTTCA 2260 	2146 GCTACCACCACCCCCCCATGGGGGGGTGGAGAGGGGTGCAAGGCCCTGCCTG	2086 ATCTAGCCAGGAATCTATTGTGTTTTTTTTTTGTGCCAATTTACTATGATTGTGTATGTGGC 2145	2026 GAGCAGAGGGGCTCACATCTCCCCTCTGATTCCCCCATGCACATTGCCTTATCTCTCCCC 2085	1966 GIGCIGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAAGGGGAAACTCTTGTGGGAG 2025 	

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US-09-146-053-3	US-09-740-041-3	US-09-385-982-354	US-09-078-294-3	US-09-078-294-4	US-08-520-373D-5	US-09-705-267A-19	PCT-US95-07201-11	US-08-367-841A-11	US-08-257-963B-11	US-09-754-250-3	US-09-813-133A-3	US-09-620-312D-884	US-09-657-474-7	US-09-268-992-7	US-09-301-665-3	US-09-791-211-3	US-09-618-166-79
Sequence 3, Appli	Sequence 3, Appli	Sequence 354, App	Sequence 3, Appli	Sequence 4, Appli	Sequence 5, Appli	Sequence 19, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 884, App	Sequence 7, Appli	Sequence 7, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 79, Appl

## ALIGNMENTS

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Sequence 4, Application US/09165868

Patent No. 6465176

GENERAL INFORMATION:
APPLICANT: Message Pharmaceuticals, Inc.
TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPOUNDS
TITLE OF INVENTION: AFFECTING RNA/RNA BINDING PROTEIN INT
FILE REFERENCE: 50093/003WO1
CURRENT APPLICATION NUMBER: US/09/165,868
CURRENT FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: PCT/US99/21672
PRIOR APPLICATION NUMBER: PCT/US99/21672
PRIOR FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 1043
TYPE: RNA
CREAKING ARTIFICIAL SCREEGE
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US-09-165-868-4/c
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Best Local Similarity 87.1%;
Matches 257; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                         1774
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CTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCCGGCCTAGA
                           CTCCGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAA 2006
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                                                                                     GGGGTTTCACCATGTTGACCAGGCTGGTTAGGAACTCCTGACCTCAAGTGATCCACCCGC
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Pred. No. 1.2e-51;
0; Mismatches 36
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RESULT 3
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1218:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS CURRENT APPLICATION DATA: APPLICATION UNDEER: US/09/016,434 FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1601 base pair:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
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ADDRESSEE: INCYTE PHARMACEUTICALS, INC
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257; Conserv
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Conservative
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Pred. No. 1.5e-51;
0; Mismatches 36;
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TITLE OF INVENTION: MCTHODS AND MATERIALS RELATING TO CD39-LIKE
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR APPLICATION NUMBER: 09/370,836
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR APPLICATION NUMBER: 09/273,447
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US-09-608-285A-59
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Patent No. 6492153
GENERAL INFORMATION:
APPLICANT: ABU-THREIDEH, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: THEREOF
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 59, Application US/09608285A Patent No. 6335013
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TYPE: DNA
ORGANISM: Human
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APPLICATION NUMBER: FILING DATE: 1999-CAPPLICATION NUMBER:
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                 1999-02-04
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Pred. No. 3.1e-50;
0; Mismatches 42
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RESULT 5
US-09-608-285A-42
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PRIOR APPLICATION NUMBER: 09/11
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 59
LENGTH: 15977
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . OTHER INFORMATION: n = a or c or g or US-09-608-285A-59
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (15702)..(158
NAME/KEY: misc feature
LOCATION: (14871)
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NAME/KEY:
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NAME/KEY:
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                                                                                                                                                                              CGGGATTTCACCACGTTGGCCAGGCTGGTCTCGAACTCCTGACCGCAAGTGATCCACCCG
                                                                                                                CCTCCGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCC
                                                                                                                                                                                                                                            TAGCTGGGAATACA--GGCACGCCACCATGCCCAGCTAATTTTTGTATTTTCAGTAGAAA
                                                                                                                                                                                                                                                                                                            CAGCTCACCGCAACCTCCACCTCCTGGGTTCAAGTGATTTTCCTGCCTCAGCCTCAGCCAAG
                                                                                                                                                          TGGGTTTCACCACGTTGGCCAGGCTGATCTCAAACTCCTGACCTCAGGTGATCCACCCG
                                                                                                                                                                                                                          TAGCTGGGATTACAGCGGTACACCACCACGCCCTGCTAATTTTTGTATTTTAGTAGAGA
                                                                                                                                                                                                                                                                                        CGGCTCACTGCAACCTCTGCCTTCCAGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAG
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ilarity 87.0%;
Conservative
                US/09608285A
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Pred. No. 1.7e-50;
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RESULT 6 US-09-557-800C-42

Sequence 42, Application US/09557800C Patent No. 6476211 GENERAL INFORMATION: APPLICANT: Ford, John APPLICANT: Mulero, Julio

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FILLE OF INVENTION: FULL TOTAL PRICE TO THE REPERENCE: 28110/36570

CURRENT APPLICATION NUMBER: US/09/608,285A

CURRENT FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: 09/583,231

PRIOR FILING DATE: 2000-05-26

PRIOR PRIOR APPLICATION NUMBER: 09/557,800

PRIOR APPLICATION NUMBER: 09/481,238

PRIOR FILING DATE: 2000-01-11

PRIOR PRIOR PRIOR NUMBER: 09/370,265

PRIOR APPLICATION NUMBER: 09/370,265

PRIOR APPLICATION NUMBER: 09/370,265

PRIOR APPLICATION NUMBER: 09/370,265

PRIOR APPLICATION NUMBER: 09/370,836

PRIOR APPLICATION NUMBER: 09/350,836

PRIOR PRIOR APPLICATION NUMBER: 09/33,447

PRIOR PILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 09/273,447

PRIOR APPLICATION NUMBER: 09/273,447

PRIOR APPLICATION NUMBER: 09/273,447

PRIOR PILING DATE: 1999-02-04

PRIOR APPLICATION NUMBER: 09/212,449

PRIOR APPLICATION NUMBER: 09/12,449

PRIOR APPLICATION NUMBER: 09/12,449

PRIOR APPLICATION NUMBER: 09/12,449

PRIOR APPLICATION NUMBER: 09/12,449

PRIOR APPLICATION NUMBER: 09/118,205

PRIOR APPLICATION NUMBER: 09/118,205

PRIOR APPLICATION NUMBER: 09/118,205

PRIOR APPLICATION NUMBER: 09/118,205

PRIOR APPLICATION NUMBER: 09/118,205

PRIOR APPLICATION NUMBER: 09/118,205

PRIOR APPLICATION NUMBER: 09/118,205

PRIOR APPLICATION NUMBER: 09/118,205

PRIOR APPLICATION NUMBER: 09/118,205

PRIOR APPLICATION NUMBER: 09/118,205

PRIOR APPLICATION NUMBER: 1998-07-16

NUMBER OF SEQ ID NOS: 60

SOFTWARE: PATEMETIN VEX: 2.0

SEQ ID NO 42

LENGTH: 14747
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (13641)
OTHER INFORMATION: n = adenosine or guanine or cytosine or thymidine
US-09-608-285A-42
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APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING
TITLE OF INVENTION: POLYPETIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.6%;
Best Local Similarity 86.6%;
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10248
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                                                                                                                                                             GGGATTTCACCACGTTGGCCAGGCTGGTCTCGAACTCCTGACCGCAAGTGATCCACCCGC 1951
                                                                                                                                                                                                                                                                                                                                                                                                                    AGCTCACCGCAACCTCCACCTCCTGGGTTCAAGTGATTTTCCTGCCTCAGCCTCCCAAGT 1833
                                                                                                                                                                                                                                                                                   AGCTGGGAATACA--GGCACGCCACCATGCCCAGCTAATTTTTGTATTTTCAGTAGAAAC 1891
                                                    CTCCGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCC
                                                                                                                      GGGGTTTCACCACGTTGGCCAGGCTGATCTCAAACTCCTGACCTCAGGTGATCCACCCGC
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Pred. No. 8.3e-50;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 14747;
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PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/122449
PRIOR FILING DATE: 1998-07-24
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/44444
PRIOR FILING DATE: 1998-07-04
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER: 05/2010 NOS: 56
NUMBER: 05/2010 NOS: 56
                                                                                                                                                                                                                          Sequence 3, Application US/09800960 Patent No. 6387677 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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FILE REFERENCE: 28110/36457
CURRENT APPLICATION NUMBER: US/09/557,800C
CURRENT FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR PILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
FILE REFERENCE: CL001158
CURRENT APPLICATION NUMBER: US/09/800,960
CURRENT FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                        APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/US99/16180 PRIOR FILING DATE: 1999-07-16
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LOCATION: (13641)
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Pred. No. 8.3e-50;
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US-08-579-445-26/c
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FILING DATE:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kirkpatrick, Anita M.
NAME: Kirkpatrick, Anita M.
REGISTRATION NUMBER: 32,617
REFERENCE/DOCKET NUMBER: STRATELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6566053
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 254;
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Best Local Similarity
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LOCATION: (1)...(62804)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Peinado, Miguel A.
APPLICANT: Ionov, Yuri
APPLICANT: Malkhosyan, Sergei
TITLE OF INVENTION: Identification of Neoplasms
TITLE OF INVENTION: of Genetic Deletions
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U
ZIP: 92660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCGGCCTCCCAAAATGCTGGGATTATAGGCGTGAGCCACCGCGCCTGGCCCAGA 13439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCCGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAA
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Peinado, Miguel A.
                                                                                                                                                                                                                                                                                                                                                Floppy disk
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                                                                                                                                                                 US/08/152,484
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                                                               STRATAG.009A
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Pred. No. 1.9e-49;
0; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ດ
                                                                                                                                                                                                                                                                                         Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by Detection
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RESULT 9
US-08-133-629-8/c
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Best Local S
Matches 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                          TELEX: 92-1742 EZEKIEL INFORMATION FOR SEQ ID NO: 6 SEQUENCE CHARACTERISTICS: LENGTH: 282 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                               REFERENCE/DOCKET NUMBER: MO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEPAX: 617-720-2441
                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Greer, Helen
REGISTRATION NUMBER: 36,816
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Munroe, David J.
APPLICANT: Housman, David E.
TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacke, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 283 base pairs
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                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/133,629
FILING DATE: 07-OCT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
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STRANDEDNESS: single
TOPOLOGY: linear
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                nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACAG--GCACGCCACCATGCCCAGCTAATTTTTGTATTTTCAGTAGAAACGGGATTTCA 1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACCTCCACCTCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCGGGTAGCTGGGAT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACCTCCACCTCCTGGGTTCAAGTGATTTTCCTGCCTCAGCCTCCCAAGTAGCTGGGAA 1842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGACGGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCGCGATCTCGGCTCACTG
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                                                                                                                                                                                                                                                                                                                                                                                                              Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                              United States of America
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pairs acid
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Pred. No. 1.5e-50;
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                                                                                                      Query Match
Best Local Similarity 86.6
Conservative
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08520373D Patent No. 6451763
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Best Local Similarity 86.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: RODITION: REPINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR FILE REPERBUCE: 2026-420JUS1
CURRENT APPLICATION NUMBER: US/08/520,373D
CURRENT FILING DATE: 1995-01-25
PRIOR APPLICATION NUMBER: 08/377,710
PRIOR FILING DATE: 1995-01-25
PRIOR APPLICATION NUMBER: 08/279,979
PRIOR APPLICATION NUMBER: 08/279,979
PRIOR PILING DATE: 1994-07-25
PRIOR PILING DATE: 1994-07-25
PRIOR PILING DATE: 1994-07-25
PRIOR PILING DATE: 1994-07-25
PRIOR PILING DATE: 1992-06-04
PRIOR APPLICATION NUMBER: 07/894,215
PRIOR APPLICATION NUMBER: 07/894,215
PRIOR APPLICATION NUMBER: 07/894,215
PRIOR APPLICATION NUMBER: 07/894,215
PRIOR PILING DATE: 1992-06-04
PRIOR APPLICATION NUMBER: 07/952,796
PRIOR PILING DATE: 1992-09-24
NUMBER: 07 SEQ ID NOS: 34
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                                                                                                                                                                                                                                                                                                       LENGTH: 14581
TYPE: DNA
ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tombran-Tink,
                                                                                                                                                                                                                        OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                          FEATURE:
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                                        9530
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1774 AGCTCACCGCAACCTCCACCTCCTGGGTTCAAGTGATTTTCCTGCCTCAGCCTCCCAAGT 1833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
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Chader, Gerald J
Becerra, Sofia P
Johnson, Lincoln V
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                                                                TTTTTTTGGAGAAGGCGTCTTGCTTTGTCACCCCACGCTGGAATGCAGTGGCGGGATCTC 1773
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                                      TTTTTTTTGAGATGGAGTCTTGCTCTGTTGCCCAGCCTGGAGTGCAGTGGCGCGATCTC
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                                                                                                                                                                                                                        mRNA: 6683; EXON: 6683-6790; EXON 11584-11675; EXON: 14539-14581; INTRON: 6791-11583; INTRON: 11676-14538; CDS: 11584-11675; 14539-14580
                                                                                                                                           9.6%;
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                                                                                                                   Score 217.8; DB 4
Pred. No. 1.6e-49;
0; Mismatches 37
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Pred. No. 1.9e-50;
5; Mismatches 30
                                                                                                                                                            DB 4;
                                                                                                                     37;
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                                                                                                                                                              Length 14581;
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  Query Match
                                        -08-367-841A-43
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-8EP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: .36434
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Chader, Gerald J.; Rodriguez, APPLICANT: Ignacio R.; Mazuruk, Krzysztof; APPLICANT: Tombran-Tink, Joyce
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ADDRESSEE: Morgan & Finnegan
                                                  LOCATION:
LOCATION METHOD:
IDENTIFICATION METHOD:
OTHER INFORMATION: seq
                                                                                                                                                                                      TYPE: Nucleac
STRANDEDNESS:
TOPOLOGY: Unk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                            MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                               LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/367,841A
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STATE: New York
                                                                                                                                        NAME/KEY: Pl-147
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                                                                                                                                                                                               Unknown
                                                                                                                                                                                                                                                                                                                                     (212) 758-4800
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DERIVED FACTOR: CHARACTERIZATION GENOMIC
ORGANIZATION AND SEQUENCE OF THE PEDF GENE
                                                      full length genomic sequence for PEDF plus flanking sequences
                                                                                                                                                                                                                                                                                                43:
                                                                                                                                                                                                                                                                                                                                                                           20264126US2
  Score 217.8;
    DB
  4;
Length 22481;
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GENERAL INFORMATION:
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                                                     TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 37-
STREET: New York
CITY: New York
TTATE: New York
                                                                                                                                                                                                                                          FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/9
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/3
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-JUN-
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chader, Gerald J.; Becerra, APPLICANT: Patricia; Schwartz, Joan P.; APPLICANT: Taniwaki, Takayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                          REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                     FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
TYPE: Nucleic Acid
STRANDEDNESS: Doub
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                                     LENGTH:
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                                     22481 Base Pairs
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                                                                                                                (212) 758-4800
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DERIVED FACTOR: CHARACTERIZATION GENOMIC
ORGANIZATION AND SEQUENCE OF THE PEDF GENE
                                                                                                                                                                                                                                                07/952,796
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0; Mismatches 37;
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US-09-875-223-2
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COTHER INFORMATION: fu
OTHER INFORMATION: se
PCT-US95-07201-43
                                                                                                                                                                                                                          ORGANISM: Homo sapiens FEATURE:
NAME/KEY: Unsure
LOCATION: 1...22484
OTHER INFORMATION: "n"
JS-09-875-223-2
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 22484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09875223 Patent No. 6391850
                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                       Matches 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Paul Gilis
TITLE OF INVENTION: Methods and Compositions for Inhibiting Angiogenesis
FILE REFERENCE: 0290-23U3
CURRENT APPLICATION NUMBER: US/09/875,223
CURRENT APPLICATION NUMBER: US 09/122,079
PRIOR APPLICATION NUMBER: US 09/122,079
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: PCT/US98/15228
PRIOR APPLICATION NUMBER: PCT/US98/15228
PRIOR APPLICATION NUMBER: WS 08/899,304
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1997-07-23
NUMBER: DF SEQ ID NOSE: 1997-07-23
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                                1714 TTTTTTTGGAGAAGGCGTCTTGCTTTGTCACCCACGCTGGAATGCAGTGGCGGGATCTC 1773
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                                                                                                           Score 217.8; DB 4;
Pred. No. 1.9e-49;
0; Mismatches 37;
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Pred. No. 1.9e-49;
0; Mismatches 37;
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                                                                                                                                                                    Length 22484;
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GENERAL INFORMATION:

APPLICANT: Gan, Weiniu

APPLICANT: Ye, Jane

APPLICANT: Ye, Jane

APPLICANT: DiFrancesco, Valentina

APPLICANT: DiFrancesco, Valentina

TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUP

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CL001194

CURRENT APPLICATION UMBER: US/09/820,002

CURRENT PILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 16
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LENGTH: 21784
TYPE: DNA
ORGANISM: HUMAN
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Best Local S
Matches 263
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NAME/KEY: misc_feature
LOCATION: (1)...(21784)
OTHER INFORMATION: n = A,T,C
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TTTTTTTAAAGAACAGAGAGGG
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Pred. No. 7.7e-49;
0; Mismatches 59;
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US-09-810-347-3

US-09-810-347-3

Sequence 3, Application US/09810347

PATENT NO. 6461847

PATENT NO. 6461847

GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

FILLE OF INVENTION: THEREOF

FILLE REFERENCE: CL001169

CURRENT APPLICATION NUMBER: US/09/810,347

CURRENT FILING DATE: 2001-03-19

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FRSTSEQ for Windows Version 4.0

SEQ ID NO
LENGTH: 42571

TYPE: DNA
ORGANISM: Human
US-09-810-347-3
Search completed: November 22, 2003, 07:54:51 Job time: 138 secs
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Best Local Similarity 86.0%;
Matches 251; Conservative
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                                                                                                                                                                                                                   1895 ATTTCACCACGTTGGCCAGGCTGGTCTCGAACTCCTGACCGCAAGTGATCCACCCGCCTC 1954
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                                                                                                                       CGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAA 2006
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Pred. No. 1.1e-48;
0; Mismatches 39; Indels 2; Gaps
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                     Score
      OLIGO_NUC
Gapop 60.0 , Gapext 60.0
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10552.029 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpna/US07
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/cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
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14 US-10-091-548-91
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Sequence 26, Appl
Sequence 1135, Ap
Sequence 1135, Ap
Sequence 11, Appl
Sequence 11, Appl
Sequence 1135, Ap
Sequence 1134, Ap
Sequence 2645, Ap
Sequence 2645, Ap
Sequence 272, Appl
Sequence 272, Appl
Sequence 10135, A
Sequence 10135, A
Sequence 10135, A
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US-09-880-107-3949	US-10-027-632-140838	US-10-027-632-140838	US-09-764-891-5924	-632-	US-10-027-632-10590	US-10-274-974-3	US-09-880-107-1992	US-10-040-862-7696	US-09-796-692-7696	US-09-864-761-16925	US-09-918-995-1933	US-10-027-632-99441	US-10-027-632-99441	7-632-	US-10-027-632-8362	US-09-864-761-87	US-10-029-386-3161	US-10-029-386-16861	US-10-029-386-2423	US-10-029-386-16123	-954		US-09-964-824A-271	US-09-918-995-11899	US-09-918-995-30086	-09-918-995-2625	US-09-918-995-22426	US-10-074-095-1134
Sequence 3949, Ap	Sequence 140838,	140838	5924, A		10590,	3, Apr		7696,		16925,	Sequence 1933, Ap	99441,	Sequence 99441, A	8362,	e 8362,	87, Apg		16861,	Sequence 2423, Ap	16123,	1369,	Sequence 973, App	271,	11899,	30086,	26257,	Ö	Sequence 1134, Ap

## ALIGNMENTS

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APPLICANT: Reddy, Roopa
APPLICANT: Reddy, Roopa
APPLICANT: Baughn, Mariah R.
APPLICANT: Baughn, Mariah R.
APPLICANT: Baughn, Mariah R.
APPLICANT: Azimzai, Yalda
TITLE OF INVENTION: FULL-LENGTH EXPRESSED GENETIC MARKERS.
TITLE OF INVENTION FULL-LENGTH EXPRESSED GENETIC MARKERS
TITLE OF TOURSTION FULL-LENGTH EXPRESSED GENETIC MARKERS.
TITLE OF TOURSTION FULL-LENGTH EXPRESSED GENETIC MARKERS.
CURRENT APPLICATION NUMBER: US/09/938,803
CURRENT APPLICATION NUMBER: 09/311,894
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PERL PROGRAM
SEQ ID NO 26
LENGTH: 2273
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte Clone 1928920
US-09-938-803-26
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                                                                                                                                                   Query Match 100.0%; Score 2273;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2273; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Yue, Henry
APPLICANT: Tang, Y. 7
APPLICANT: Lal, Preet
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GGGCTCCCGGAGTTAAGATGGCGTCCTCAGCGGAGGGGACGAGGGGACTGTGGTGGCGC
                                                                                         Tang, Y. To
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221 CTGTATTAGATAAARCACTTCTGTTTGTTCAGTTTTTCAAAAAAAAAA	Db	1141 TCCTTGGAAATAAAGAACTCTCTCAGGGTCTCTCGTTGCTATTCCTGGCCCTCTGGCACG 1200	
0-0	Db (2)	1081 CCTCATTCAACACCACCAACGCCTGGGTGGCCCGCTACATCTTCAAACGACTCAAGT 1140	
	g 4g	1021 CCTGTGCCAACATGAAGGTGTGGCTCTTTGAAACAAACCCCCGCTTCACTGGCACCATTG 1080	
- a-a	⊋	961 GCATTTTGACGGGCCTGGGCTTCAATĠGCTTTGAAGAAAAGGGCAAGGCAA	
GCGTGAGCCACCGTGCCCGGCCCAAAGGGGAAACTCTTGTGGGAGGAGCACAG 	Db Qy	901 TCTGGGGCAAGTTTGTGCTGTACAAATATGTCACCTGTTGGCTGGTCACAGAAGGAGTAT 960 	
, H—H	) B Q	841 ATCTCCTCACTGAAGACTATGACAACCACCCCTTCTGGTTCCGCTGCATGTACATGCTGA 900	
61 -0	לע לע	781 GTCTGGGCCTTTTCTACCTAGTGGGCTACACAGCTGCTCAGCCCCACATCACAGAAGACT 840	
	d dd	721 AGCTGATTGACATACCAGGAAAGATACCAAACAGCATCATTCCTGCTCTAAGCGCCTGA 780	
ີ 1 1 ດ—ດ	y da	661 GGGCCTTCTTGGTAGGGCCCCAGTTCTCAATGAATCACTACATGAAGCTGGTGCAGGGAG 720	
· »—»	Qγ	601 AATATGCCATACGTGGTGTTCCTTCCCTGGCTGGAAGTTGCTGGTTTCTCCTACTTCTATG 660	
0-0	D CY	541 TGGCTGTTGACTACTTTGACGGAGGGAAAGATCAGAATTCCTTGTCCTCTGAGCAACAGA 600	
a—a	) p Q	481 GCAACTACGATATCAAGTGGACAATGCCACATTGTGTTCTGAACTTTGAAGCTGATTGGTT 540	
2 2 2	אַ סם אַ	421 TCACTACCTTTTGCTTCCAGATGGCCTACCTTCTGGCTGG	
4 5	) p 4	361 TGTGTATTGTGCTTCAGTTCCTCATCCTTCGACTAATGGGCCGCACCATCACTGCCGTCC 420	
, 10—6	ב אם אם	301 CCTTTACAGGCCTCTCAATTGCTTATTTTAACTTTGGAAACCAGCTCTACCACTCCCTGC 360 	
) H—	D 4	241 CTTTGTTTTATCGGCATTACCTTTTCTACAAGGAGACCTACCT	
T261 GACAGGETCATGETCATGETCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	Q	181 TGGGCGCGTCAGAACAGGCGCTGCGGCTGATCATCTCCCATCTTCCTGGGTTACCCCTTTG 240	
. ດ~-c	) Q	121 TGGCGGGGGTTCTGCAGTCGGGTTTCCAGGAGCCTGAGCCTTAACAAGTTGGCGACGTCCC 180	
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US-09-880-107-3415
; Sequence 3415, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: HORROR
; APPLICANT: Vockley, Joseph G.
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SEQ ID NO 3415
LENGTH: 1842
TYPE: DNA
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No.
-09-880-107-3415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
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                                                AGCCCCCACATCACAGAAGACTATCTCCTCACTGAAGACTATGACAACCACCCCTTCTGG
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    TTCCGCTGCATGTACATGCTGATCTGGGGCAAGTTTGTGCTGTACAAATATGTCACCTGT
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100.0%; Pred. No. 0;
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RESULT 4
US-09-764-860-1135/c
Sequence 1135, Application US/09764860
Patent No. US2002099953A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and FILE REFERENCE: PC008
CURRENT APPLICATION NUMBER: US/09/764,860
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or NUMBER OF SEQ ID NOS: 1198
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1135
LENGTH: 7461
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: ROSen et al.
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PA122
CURRENT APPLICATION UNUMBER: US/09/764,904
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM O:
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 91
LENGTH: 7461
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; ORGANISM: Homo sapiens
US-09-764-904-91
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US-09-764-904-91/c
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Patent No. US20020173454A1
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 91
LENGTH: 7461
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ORGANISM: Homo sapiens
-10-091-548-91
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA122C1
CURRENT APPLICATION NUMBER: US/10/091,548
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 137
Prior Application removed - See File Wrapper
SOFTWARE: PatentIn Ver. 2.0
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RESULT 7
US-10-074-095-1135/c
; Sequence 1135, Application US/10074095
; Sequence 1005-10074095 PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04 CURRENT APPLICATION NUMBER: US/10/074,095
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 09/764,860 TITLE OF INVENTION: Nucleic FILE REFERENCE: PC008C1 OR FILING DATE: 2000-07-14
OR APPLICATION NUMBER: 60/225,757
OR APPLICATION NUMBER: 60/226,868
OR FILING DATE: 2000-08-12
OR APPLICATION NUMBER: 60/216,647
OR APPLICATION NUMBER: 60/216,647
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OR APPLICATION NUMBER: 60/251,869
OR APPLICATION NUMBER: 60/251,869
OR APPLICATION NUMBER: 60/251,869 OR APPLICATION NUMBER: 60/214,886
OR FILING DATE: 2000-06-28
OR APPLICATION NUMBER: 60/217,487
OR FILING DATE: 2000-07-11
OR APPLICATION NUMBER: 60/225,758
OR APPLICATION NUMBER: 60/220,963
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OR APPLICATION NUMBER: 60/217,496 OR FILING DATE: 2000-09-21

R APPLICATION NUMBER: 60/234,223

DR FILING DATE: 2000-09-21

DR APPLICATION NUMBER: 60/228,924

DR FILING DATE: 2000-08-30

DR APPLICATION NUMBER: 60/224,518 APPLICATION NUMBER: 60/225,447
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/218,290 FILING DATE: 2000-12-08
APPLICATION NUMBER: 60/235,834
FILING DATE: 2000-09-27 APPLICATION NUMBER: 60/234,274 Acids, Proteins, and Antibodies

OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/236,369
OR FILING DATE: 2000-09-29
OR APPLICATION NUMBER: 60/224,519
OR FILING DATE: 2000-08-14
OR FILING DATE: 2000-07-26
OR APPLICATION NUMBER: 60/240,964
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/241,809
OR APPLICATION NUMBER: 60/249,299
OR FILING DATE: 2000-11-17
OR APPLICATION NUMBER: 60/249,299
OR FILING DATE: 2000-11-17
OR APPLICATION NUMBER: 60/236,327

DR FILING DATE: 2000-09-29

R APPLICATION NUMBER: 60/241,785

DR FILING DATE: 2000-10-20

DR APPLICATION NUMBER: 60/244,617

DR FILING DATE: 2000-11-01

DR APPLICATION NUMBER: 60/225,268

R FILING DATE: 2000-08-14

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OR APPLICATION NUMBER: 60/251,868
OR FILING DATE: 2000-12-08
OR APPLICATION NUMBER: 60/25,868
OR APPLICATION NUMBER: 60/234,997
OR FILING DATE: 2000-09-01
OR APPLICATION NUMBER: 60/229,343
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OR APPLICATION NUMBER: 60/229,287
OR FILING DATE: 2000-09-01
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OR FILING DATE: 2000-09-05
OR APPLICATION NUMBER: 60/23,536
OR APPLICATION NUMBER: 60/237,039
OR FILING DATE: 2000-09-08
OR APPLICATION NUMBER: 60/237,039
OR FILING DATE: 2000-10-02
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OR APPLICATION NUMBER: 60/237,037
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GENERAL INFORMATION:

APPLICANT: Rosen et al.

FILLE OF INVENTION: Nucleic Acids, Proteins, and FILLE REFERENCE: PA128

CURRENT APPLICATION NUMBER: US/09/908,711

CURRENT APPLICATION NUMBER: US01/01360

PRIOR APPLICATION NUMBER: US01/01360

PRIOR FILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: 09/764,867

PRIOR APPLICATION NUMBER: US01/01344

PRIOR APPLICATION NUMBER: US01/01344

PRIOR FILING DATE: 2001-01-17
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Patent No. US20020045230A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/231,243
FILING DATE: 2000-09-08
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TYPE: DNA
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                                                                                                     NUMBER OF SEQ ID NOS: 167
                                                                                                                    PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/209,467
PRIOR FILING DATE: 2000-06-07
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APPLICATION NUMBER: 60/179,065
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FILING DATE: 2001-01-17
APPLICATION NUMBER: US01/01347
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APPLICATION NUMBER: US01/01348
FILING DATE: 2001-01-17
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APPLICATION NUMBER: 09/764,902
FILING DATE: 2001-01-17
APPLICATION NUMBER: US01/01239
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FILING DATE: 2001-01-17
APPLICATION NUMBER: 09/764,898
FILING DATE: 2001-01-17
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APPLICATION NUMBER: US01/01340
FILING DATE: 2001-01-17
APPLICATION NUMBER: 09/764,874
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APPLICATION NUMBER: US01/01341
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APPLICATION NUMBER: 09/764,896
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APPLICATION NUMBER: US01/01329
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APPLICATION NUMBER: US01/01349
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NAME/KEY: SITE
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RESULT 10

US-09-764-877-2645/c

US-09-764-877-2645/c

Sequence 2645, Application US/09764877

Patent No. US20020147140A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Ant:
FILE REFERENCE: PC005

CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or fil
NUMBER OF SEQ ID NOS: 4031

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2645

LENGTH: 32174

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Sequence 232, Application US/09860670

Patent No. US20020165137A1

GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA127P1
CURRENT APPLICATION NUMBER: US/09/860,670
CURRENT FILING DATE: 2001-05-21
Prior application data removed - consult PAL
NUMBER OF SEQ ID NOS: 289
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LENGTH: 32174
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Sequence 90, Application US/09764904
Patent No. US20020173454A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, an FILE REFERENCE: PA122
CURRENT APPLICATION UNMBER: US/09/764,904
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION data removed - consult PALM conumber of SEQ ID NOS: 137
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 90
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TYPE: DNA
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LOCATION:
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RESULT 14
US-09-764-891-10135
Sequence 10135, Application US/09764891
Publication No. US200300778008A1
Publication No. US200300778008A1
Publication No. US200300778008A1
PULSON INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
UNMBER OF SEQ ID NOS: 10231
NUMBER: OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0

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SEQ ID NO 10135

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TYPE: DNA

ORGANIAM: Homo sapiens

FEATURE:
NAME/KEY: SITE
LOCATION: (1296)
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NAME/KEY: SITE
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Sequence 10179, Application US/09764891 Publication No. US20030077808A1 GENERAL INFORMATION: Prior application data removed -NUMBER OF SEQ ID NOS: 10231 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 10179 LENGTH: 32174 CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17 APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, FILE REFERENCE: PC006 n equals a,t,g, equals equals equals equals a,t, equals equals equals a,t,g, equals equals a,t, a,t, a,t, a,t,g, a,t,g, a,t,g, a,t,g, ò ū ġ Ď consult PALM Proteins, 유 ů, õ or ဝူ 9 or r o F and õ file wrapper Antibodies

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	, App1	10,	Sequence	US-09-798-096-10	4	99500	2.1	47	35		
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	Appli	4	Sequence	US-08-520-373D-4	4	14581	2.1	47	29	ი	
	, Appl	27,	Sequence	US-09-679-729-27	4	12146	2.1	47	28	ი	
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PRIOR APPLICATION NUMBER: 2002-05-06
PRIOR FILING DATE: 2002-05-06
PRIOR FILING DATE: 2000-02-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 74962
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME OF SEQ ID NO SAPIEN GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerritsen, Mary E. ; NAME/KEY: misc\_feature; ICCATION: (1)...(74962); OTHER INFORMATION: n = A,T,C US-09-685-853A-3 US-09-996-243-398/c Sequence 3, Application US/09685853A
PATENT NO. 6479270
GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al.
APPLICANT: WEI, Ming-Hui et al.
APPLICANT: WEI, MING-Hui et al.
APPLICANT: WEI, MING-Hui et al.
APPLICANT: WEI, MING-Hui et al.
APPLICANTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOOG871
CURRENT APPLICATION NUMBER: US/09/685,853A
CURRENT FILING DATE: 2002-05-06 sequence 398, Application US/09996243
Patent No. 6478825 APPLICANT: 62149 GCAACCTCCACCTCCTGGGTTCAAGTGATTTTCCTGCCTCAGCCTCCCAAGTAGCTGGG 1782 GCAACCTCCACCTCCTGGGTTCAAGTGATTTTCCTGCCTCAGCCTCCCAAGTAGCTGGG 1840 h 2.6%; Score 59; DB Similarity 100.0%; Pred. No. 9.: 59; Conservative 0; Mismatches Gerber, Hanspeter Gerritsen, Mary E Ferrara, Napoleone õ Q DB 4; L.
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CURRENT FILING DATE: 2001-11-14
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TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TILE OF INVENTION: Acids Encoding the Same
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FILING DATE: 1998-05-07
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FILING DATE: 1997-11-13
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                                           FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212
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FILING DATE: 1998-06-04
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Roy, Margaret Ann
Stewart, Timothy
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Grimaldi, J. Christopher
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APPLICATION NUMBER: 60/090429 APPLICATION NUMBER: 60/090252 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090254 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952 APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19 FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089801
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APPLICATION NUMBER: FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/

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APPLICATION NUMBER: 60/090557

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LENGTH: 17
TYPE: DNA
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Matches 49
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                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/804,471A CURRENT FILING DATE: 2001-03-13 NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                             APPLICANT: WEBSTER, Marion et al TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, TITLE OF INVENTION: THEREOF
                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                 FILE REFERENCE: CL001164
NAME/KEY: misc_feature
LOCATION: (1)...(174493)
OTHER INFORMATION: n = F
                                                                   ORGANISM: Human
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FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/090863
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APPLICATION NUMBER: 60/091626
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US-09-702-705-321
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APPLICANT: Wang, T
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APPLICANT: Heartlein, Michael W.
APPLICANT: Selden, Richard F
APPLICANT: Selden, Richard F
TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
FILE REFERENCE: 07236/017001
CURRENT APPLICATION NUMBER: US/09/305,384
CURRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: US 60/084,649
EARLIER FILING DATE: 1998-05-07
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CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
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APPLICANT: Retter, Marc
APPLICANT: Mention, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
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Lodes, Michael A.
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Vedvick, Tom
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Pred. No. 2.1e-11;
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Pred. No.
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2.4e-12;
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                                                                                                           Length 2280;
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RESULT 6
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; ORGANISM: Homo sapiens
US-09-736-457-321
                                                   ; TYPE: DNA; ORGANISM: Homo sapiens US-10-045-428A-9
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TITLE OF INVENTION: Promoter
FILE REFERENCE: 50026/011003
CURRENT APPLICATION NUMBER: US/10/045,428A
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: 09/735,103
PRIOR APPLICATION NUMBER: 09/142,529
PRIOR APPLICATION NUMBER: 09/142,529
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-08-12
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Best Local Similarity
Matches 47; Conserv
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Query Match
Best Local Similarity
                                                                                                                           SOFTWARE: I
SEQ ID NO 9
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CURRENT FILING DATE: 2000-12-13
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APPLICANT: Sakata, Tsuneaki
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APPLICANT: Wang, Aijun
BITLE OF INVENTION: COMPOSITIONS AND METHODS
BITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
BITLE REFERENCE: 210121.478C15
                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/JP97/00741
PRIOR FILING DATE: 1997-03-10
                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                  PRIOR FILING DATE:
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                                                                                                        ENGTH:
                                                                                                                                                                                                   FILING DATE: 1997-03-10 APPLICATION NUMBER: JP 8/54294
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Carter, Darrick
Retter, Marc
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Bangur, Chaitanya S.
Lodes, Michael A.
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Tabata, Toshiaki
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Pred. No.
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. 2.1e-11;
   DB 4; L. 2.1e-11;
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                  Length 3129;
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US-09-305-384-1/c

Sequence 1, Application US/09305384 Patent No. 6242218

GENERAL

INFORMATION

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TYPE: DNA
CRGANISM: Homo sapiens
US-09-305-384-5
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Best Local Similarity
Matches 47; Conserv
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Patent No. 6569681
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LENGTH: 6235
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CURRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: US 60/084,649
EARLIER FILING DATE: 1998-05-07
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SOFTWARE: FastSEQ for Windows Version 3.0
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FILE REFERENCE: 07236/017001
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NPPLICANT: Selden, Richard F
                                                                                                                                                                                                                         OFTWARE:
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                                                                                                                                                                                                                                                      URRENT APPLICATION NUMBER:
URRENT FILING DATE: 2000-0
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                                                                                                                                                   GANISM: Homo sapiens
                                                                                                                                                                                                                                                                                      西原ANT: Ivanov, Evguenii
地區 OF INVENTION: METHODS OF IMPROVING HOMOLOGOUS RECOMBINATION
E REFERENCE: 10278/016001
                                                                               Local
                                                                                                                                                                                                      ID NO 6
                                                                                                      Match
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5251 GCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCC 5205
                               1956 GCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCC 2002
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Patent No. 6569681
GENERAL INFORMATION:
APPLICANT: Ivanov, Evguenii
TITLE OF INVENTION: METHODS OF IMPROVING HOMOLOGOUS RECOMBINATION
FILE REFERENCE: 10278/016001
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Best Local Similarity
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CURRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: US 60/084,649
EARLIER FILING DATE: 1998-05-07
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                  MEDIUM TYPE: Floppy
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                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                    COUNTRY: USA
                                                                                                                                       ADDRESSEE:
                                                                                                         TY: New York
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                                                                                       New York
                                                                                                                                                                                                                                                                                                                                                 Application US/08257963B
                                                                                                                     345 Park Avenue
                                                                                                                                                                                                                                                        Chader, Gerald J.; Becerra, S. Patricia; Schwartz, Joan P.; Taniwaki, Takayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
: Floppy Disk
IBM PC Compatible
                                                                                                                                      Morgan & Finnegan
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-03-14
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                                                                                                                                                                                                           DERIVED FACTOR: CHARACTERIZATION OF ITS NOVEL BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
                                                                                                                                                                                                                                           PIGMENT EPITHELIUM
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Pred. No. 2e-11;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/08367841A Patent No. 6319687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                        SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 24-SEPT
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PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION METHOD: OTHER INFORMATION: 7. OTHER INFORMATION: De
                            APPLICATION NUMBER: FILING DATE: 30-DEC
                                                                                                                                                                                                     CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                      STREET:
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TORNEY/AGENT INFORMATION:
                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: JT106
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                                                                                                                                                                                                                                 ADDRESSEE:
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IBRARY: DASH II
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MATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1956 GCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCC 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PÉRENCE/DOCKET NUMBER: 20
SCOMMUNICATION INFORMATION:
SLEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5615 GCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCC 5569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47;
                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
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DEDNESS: Double
                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOROTHY R. AUTH
                                                                                                                                                                                                                                                                                   INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7210 Base Pairs
                                                                                                                                                                                                                      345 Park Avenue
                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (212)
                                                                                                                                                                                                                                                                                                                                                           Chader,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown
                                                                                                                                                                                                                                                                                                                                             Ignacio R.; Mazuruk, Krzysztof;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WORDPERFECT 5
                                                                                                                                                                                                                                   Morgan
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                            30-DEC-1994
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                                                                                                                                                                                                                                & Finnegan
                                                                                                                                                                                                                                                                                                             PIGMENT EPITHELIUM
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                                          US/08/367,841A
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Pred. No.
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om human placental genomic DNA
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Gaps

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/952,796

24-SEP-1992

APPLICATION NUMBER: FILING DATE: 07-JUN

07-JUN-1994

08/257,963

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SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Patricia, APPLICANT: Taniwaki, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
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NAME: DOROTHY R. AUTH
                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Huma
                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                  CURRENT APPLICATION DATA:
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OTHER INFORMATION:
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                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                 APPLICATION NUMBER: PCT/FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: JT6A
LOCATION:
                                                                                CLASSIFICATION:
                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                     IDDRESSEE:
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                                                                                                                                                                                                                                                                                    New York
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Nucleic Acid
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                                                                                                                                                                                                                                                                   New York
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                                                                                                                                                                                                                                                                                                      345 Park Avenue
                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                     Chader, Gerald J.; Becerra, Sofia Patricia; Schwartz, Joan P.; Taniwaki, Takayuki
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                                                                                                                                                   WORDPERFECT 5.1
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                                                                                                                                                                                                                                                                                                                     Morgan & Finnegan, L.L.P.
                                                                                                                                                                                                  Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic DNA
                               30-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Double
                                                                                                                                                                                                                                                                                                                                                                    DERIVED FACTOR: CHARACTERIZATION GENOMIC ORGANIZATION AND SEQUENCE OF THE PEDF GENE
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                                                                                                                                                                                                                                                                                                                                                                                                     PIGMENT EPITHELIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.0 kb No. 6319687 1-No. 6319687 fragment; Derived from human placental genomic DNA; also referred to as JT106
                                                  08/367,841
                                                                                                                    ·PCT/US95/07201
08/257,963
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Matches 47; Conserv
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PRIOR APPLICATION DATA:
CLASSIFICATION: 514
ATTORNEW/AGENT WNFORMATION:
NAME: Smith, William M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
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IMMEDIATE SOURCE:
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                                                                           CURRENT APPLICATION DATA:
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                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                           SOFTWARE:
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LOCATION:
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OTHER INFORMATION:
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                                                                                                        ©OMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                     STATE: Cal
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                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                               DRESSEE:
                                                                                                                                                                                                                                                            ESPONDENCE ADDRESS:
                                                                                                                                                                        94111-3834
                                                                                                                                                                                                                  San Francisco
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                                                                                                                                                                                                                                                                                            INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                pplication US/08652265
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Two Embarcadero Center, Eighth Floor
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                                                                                        PatentIn Release #1.0,
                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                         Gnirke, Andreas
Ruddy, David
                                                                                                                                                                                                                                                                                                                                                                    Drayna, Dennis T.
Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                  Floppy disk
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                                             23-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.0 kb Not 1-Not fragment; Derived from human placental genomic DNA; also referred to as JT106
                                                           US/08/652,265
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Pred. No.
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                                                                                          Version #1.30
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REGISTRATION NUMBER:

17957-000500

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Search completed: November 22, 2003, 14:01:17 Job time : 137 secs
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Best Local Similarity luv.
Thes 47; Conservative
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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LOCATION: 5507..602
OTHER INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 140..7319
OTHER INFORMATION: //
OTHER INFORMATION: no
OTHER INFORMATION: cl
                                                                                                                                                                                                                                 LOCATION: replace (5834, "g")
OTHER INFORMATION: /phenotyp
OTHER INFORMATION: /label= 2
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OTHER INFORMATION: /phenotyp
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OTHER INFORMATION: /phenotyp
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RMATION: /product= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                         2.1%; Score 47;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "start and stop positions for normal or wild-type (unaffected) genomic sequence surrounding variant for 24d1(G) allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indee "start and stop positions for normal or wild-type (unaffected) genomic sequence surrounding variant for 24d2(C) allele (SEQ ID NO:41)"
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(unaffected)"
/label= 24d2
                                                                                                                                                                                                                               /phenotype= "normal or wild-type
(unaffected)"
/label= 24d1
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(unaffected)"
/label= 24d7
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normal or wild-type (unaffected) allele
cDNA (SEQ ID NO:9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "No. 6025130mal or wild-type (unaffected) Hereditary Hemochromatosis (HH) gene allele"
                                                                                                                                        0,
                                                                                                                                          Mismatches
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2e-11;
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                                                                                                                                                                          Length 10825;
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                                                                                                                                       0;
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